NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV

Background of the Invention

This invention relates generally to immunoassays for the detection and differentiation of antibodies to Human Immunodeficiency Virus Type 1 (HIV-1) Group M, HIV-1 Group O and Human Immunodeficiency Virus Type 2 (HIV-2). More particularly, the invention relates to novel antigen constructs useful as reagents in such assays, as well as polynucleotides, DNA clones, expression vectors, transformed host cells and the like which are useful in the preparation of such antigens.

Detection of HIV infection in a patient, and characterization of the viral type, are typically carried out using immunoassays which rely on the highly specific interaction between antigens used as reagents in the assay and circulating antibodies in the patient's serum. The immunoreactivity of patient antibodies with some antigens, and to a lesser extent or not at all with others, permits the identification of the type and subtype of the HIV which is present.

Currently, there are two major phylogenetic groups of HIV-1 designated as Groups "M" and "O." G. Meyers et al., *Human Retroviruses and AIDS 1995*, Los Alamos National Laboratory, Los Alamos, NM (1995). HIV-1 Group M isolates further have been divided into subgroups (A to J) that are phylogenetically approximately equidistant from each other. Group M isolates predominate worldwide. The earliest reports about the sequence of HIV-1 Group O indicated that these viruses were as closely related to a chimpanzee virus as to other HIV-1 subgroups. See, for example, L.G. Gürtler et al., *J. Virology* 68:1581-1585 (1994); M. Vanden Haesevelde et al., *J. Virology* 68:1586-1596 (1994); De Leys et al., *J. Virology* 64:1207-1216 (1990); DeLeys et al., U.S. Patent No. 5,304,466; L.G. Gürtler et al., European Patent Publication No. 591914 A2. The Group O sequences are the most divergent of the HIV-1 sequences described to date. Although HIV-1 Group O strains are endemic to west central Africa (Cameroon, Equatorial Guinea, Nigeria and Gabon), patients infected with Group O isolates now have been identified in Belgium, France, Germany, Spain and the United States. See, for example, R. DeLeys et al., *supra*; P. Charneau et al., *Virology* 205:247-253 (1994); I. Loussert-Ajaka et al., *J. Virology* 69:5640-5649 (1995); H. Hampl et al., *Infection* 23:369-370 (1995); A. Mas et al., *AIDS Res. Hum. Retroviruses* 12:1647-1649 (1996); M. Peters et al., *AIDS* 11:493-498 (1997); and M.A. Rayfield et al., *Emerging Infectious Diseases* 2:209-212 (1996).

HIV-1 Group M serology is characterized in large part by the amino acid sequences of the expressed viral proteins (antigens), particularly those comprising the core and envelope (env) regions. As between various strains of this rapidly-mutating virus, these antigens are structurally and functionally similar but have divergent amino acid sequences which elicit antibodies that are similar but not identical in their specificity for a particular antigen.

One of the key serological targets for detection of HIV-1 infection is the 41,000 MW transmembrane protein (TMP), glycoprotein 41 (gp41). gp41 is a highly immunogenic protein which elicits a strong and sustained antibody response in individuals considered seropositive for HIV. Antibodies to this protein are among the first to appear at seroconversion. The immune response to gp41 apparently remains relatively strong throughout the course of the disease, as evidenced by the near universal presence of anti-gp41 antibodies in asymptomatic patients as well as those exhibiting clinical stages of AIDS. A significant proportion of the antibody response to gp41 is directed toward a well-characterized immunodominant region (IDR) within gp41.

Infections with HIV Type 2 (HIV-2), a virus initially found in individuals from Africa, now have been identified in humans outside of the initial endemic area of West Africa, and have been reported in Europeans who have lived in West Africa or those who have had sexual relations with individuals from this region. See, for example, A.G. Saimot et al., *Lancet* i:688 (1987); M. A. Rey et al., *Lancet* i:388-389 (1987); A. Werner et al., *Lancet* i:868-869 (1987); G. Brucker et al., *Lancet* i:223 (1987); K. Marquart et al., *AIDS* 2:141 (1988); CDC, MMWR 37:33-35 (1987); Anonymous, *Nature* 332:295 (1988). Cases of AIDS due to HIV-2 have been documented world-wide. Serologic studies indicate that while HIV-1 and HIV-2 share multiple common epitopes in their core antigens, the envelope glycoproteins of these two viruses are much less cross-reactive. F. Clavel, *AIDS* 1:135-140 (1987). This limited cross-reactivity of the envelope antigens is believed to explain why currently available serologic assays for HIV-1 may fail to react with certain sera from individuals with antibody to HIV-2. F. Denis et al., *J. Clin. Micro.* 26:1000-1004 (1988). Recently-issued U.S. Patent No. 5,055,391 maps the HIV-2 genome and provides assays to detect the virus.

These viral strains are, for the most part, readily identified and characterized using commercially-available diagnostic tests. However, concerns have arisen regarding the capability of currently-available immunoassays, designed for the detection of antibody to HIV-1 (Group M) and/or HIV-2, to detect the presence of antibody to HIV-1 Group O. I. Loussert-Ajaka et al., *Lancet* 343:1393-1394 (1994); C.A. Schable et al., *Lancet* 344:1333-1334 (1994); L. Gürtler et al., *J. Virol. Methods* 51:177-184 (1995). Although, to date, few patients outside of west Central Africa have been found to be infected with HIV-1 Group O isolates, health officials fear the emergence of this subtype in other geographic areas as well.

Consequently, there is a continued need for new antigens, suitable for use in immunoassays, which alone or in conjunction with other antigens permit the recognition of all HIV-1 (Group M and Group O) and HIV-2 isolates and/or infections.

Summary of the Invention

It has now been found that certain polypeptides or combinations of are particularly useful in the detection of HIV-1 Group O and other HIV infections. Consequently, in a first aspect of the present invention is disclosed an isolated HIV-1 Group O *env* polypeptide having an amino acid sequence consisting essentially of the sequence of Figure 1 (SEQ ID NO:61), representing the full-length *env* region of the HIV-1 Group O isolate HAM112. Similarly disclosed is an isolated HIV-1 Group O *env* polypeptide comprising an immunoreactive portion of the above full-length polypeptide, as well as polynucleotides encoding such polypeptides.

In a second aspect of the present invention, an antigen construct is disclosed which comprises a first HIV-1 Group O *env* polypeptide fused to a second HIV-1 Group O *env* polypeptide. Preferably, the first polypeptide of such an antigen construct is a gp120 polypeptide and the second polypeptide is a gp41 polypeptide, optionally with a portion of the hydrophobic region of the gp41 polypeptide being deleted so as to facilitate expression when expressed as a recombinant product. Also preferred among the above antigen constructs are those in which at least one of the first and second HIV-1 Group O *env* polypeptides is derived from HIV-1 Group O isolate HAM112, as are those in which the first polypeptide comprises an immunoreactive portion of the gp120 protein of HIV-1 Group O isolate HAM112.

In the above Group O *env* constructs, the first polypeptide may have an amino acid sequence which consists essentially of residues 1 through 520 of the sequence shown in Figure 1 (SEQ ID NO:61), or alternatively an immunoreactive portion thereof. A shortened and preferred first polypeptide is one having an amino acid sequence consisting essentially of residues 476 through 520 of the sequence of Figure 1 (SEQ ID NO:61). Along with any of the above polypeptides, the second polypeptide used in the constructs of the invention may be an immunoreactive portion of the gp41 protein of HIV-1 Group O isolate HAM112, from which a portion of the hydrophobic region of the gp41 protein of HIV-1 Group O isolate HAM112 is optionally absent. In particular, the deleted portion may be that part of gp41 which has an amino acid sequence consisting essentially of residues 690 through 715 of the sequence of Figure 1 (SEQ ID NO:61).

The above second polypeptide will preferably have an amino acid sequence consisting essentially of residues 521 through 873 of the sequence of Figure 1 (SEQ ID NO:61) or a portion thereof. More preferably, the second polypeptide may have an amino acid sequence consisting essentially of residues 47 through 373 of Figure 9 (SEQ ID NO:52); still more preferably, the amino acid sequence may consist essentially of residues 47 through 245 of Figure 7 (SEQ ID NO:48); and even more preferably, the amino acid sequence may consist essentially of residues 47 through 215 of Figure 5 (SEQ ID NO:58). Representative of the Group O *env* constructs of the invention are constructs pGO-8PL, pGO-8CKS, pGO-9PL, pGO-9CKS, pGO-11PL and pGO-11CKS, as well as any derivatives, variants and analogs thereof.

In a further aspect of the present invention, there is disclosed an antigen construct comprising a fusion of at least one HIV-1 Group O *env* polypeptide with at least one HIV-1 Group M *env* polypeptide, and more preferably an antigen construct comprising a fusion of:

(a) a first HIV-1 Group O *env* polypeptide;

(b) a second HIV-1 Group O *env* polypeptide;

(c) a first HIV-1 Group M *env* polypeptide; and

(d) a second HIV-1 Group M *env* polypeptide.

The HIV-1 Group M polypeptides in the above constructs may be derived from an HIV-1 isolate of Subtype B, and preferably at least one is derived from HIV-1 Group M isolate HXB2R. In any of these Group O/Group M *env* constructs, at least one of the HIV-1 Group O sequences may be derived from HIV-1 Group O isolate HAM112.

More particularly, the first Group O *env* polypeptide and the first Group M *env* polypeptide may both be gp120 polypeptides, while the second Group O *env* polypeptide and the second Group M *env* polypeptide may both be gp41 polypeptides. To enhance expression, a portion of the hydrophobic region of at least one of the gp41 polypeptides may be deleted.

Antigen constructs included among the above are those in which:

(a) the first HIV-1 Group O *env* polypeptide comprises an immunoreactive portion of the gp120 protein of HIV-1 Group O isolate HAM112;

(b) the second HIV-1 Group O *env* polypeptide comprises an immunoreactive portion of the gp41 protein of HIV-1 Group O isolate HAM112

(c) the first HIV-1 Group M *env* polypeptide comprises an immunoreactive portion of the gp120 protein of a first HIV-1 Group M isolate of Subtype B; and

(d) the second HIV-1 Group M *env* polypeptide comprises an immunoreactive portion of the gp41 protein of a second HIV-1 Group M isolate of Subtype B.

Preferred among these are constructs wherein the first and second HIV-1 Group M isolates of Subtype B are the same and are HIV-1 Group M isolate HXB2R, as well as those wherein a portion of the hydrophobic region of the gp41 protein of HIV-1 Group M isolate HXB2R is absent from the second HIV-1 Group M *env* polypeptide.

Preferred Group O/Group M *env* constructs include those in which (a) the first HIV-1 Group M *env* polypeptide has an amino acid sequence consisting essentially of residues 251 through 292 of the sequence of Figure 12 (SEQ ID NO:108), and (b) the second HIV-1 Group M *env* polypeptide has an amino acid sequence consisting essentially of residues 293 through 599 of the sequence of Figure 12 (SEQ ID NO:108) or a portion thereof. Especially preferred are those in which the second HIV-1 Group M *env* polypeptide has an amino acid sequence consisting essentially of residues 293 through 492 of the sequence of Figure 12 (SEQ ID NO:108).

Also preferred are the above Group O/Group M *env* constructs in which the first HIV-1 Group O *env* polypeptide has an amino acid sequence consisting essentially of residues 1

through 520 of the sequence of Figure 1 (SEQ ID NO:61) or a portion thereof, and especially those comprising a first HIV-1 Group O *env* polypeptide which has an amino acid sequence consisting essentially of residues 476 through 520 of the sequence of Figure 1 (SEQ ID NO:61). The second HIV-1 Group O *env* polypeptide may be one having an amino acid sequence consisting essentially of residues 521 through 873 of the sequence of Figure 1 (SEQ ID NO:61) or a portion thereof, from which a portion of the hydrophobic region of the gp41 protein of HIV-1 Group O isolate HAM112 may optionally be absent. Preferred constructs are those in which such second HIV-1 Group O *env* polypeptides have an amino acid sequence consisting essentially of residues 47 through 373 of Figure 9 (SEQ ID NO:52); more preferred are those in which the second HIV-1 Group O *env* polypeptide has an amino acid sequence consisting essentially of residues 47 through 245 of Figure 7 (SEQ ID NO:48); and even more preferred are those in which the second HIV-1 Group O *env* polypeptide has an amino acid sequence consisting essentially of residues 47 through 215 of Figure 5 (SEQ ID NO:58). Representative of the Group O/Group M *env* constructs of the invention are constructs pGO-12CKS, pGO-13CKS and pGO-14PL, and derivatives, variants and analogs thereof.

In yet another aspect of the present invention, an antigen construct is disclosed which comprises a fusion of a first HIV-1 *env* polypeptide, a second HIV-1 *env* polypeptide, and at least one additional HIV-1 polypeptide, and especially one in which each such HIV-1 *env* polypeptides are HIV-1 Group O polypeptides. The first HIV-1 Group O *env* polypeptide of this construct may be a gp120 polypeptide, and the second HIV-1 Group O *env* polypeptide a gp41 polypeptide. More particularly, the first HIV-1 Group O *env* polypeptide of this construct may comprise an immunoreactive portion of the gp120 protein of HIV-1 Group O isolate HAM112, while the second HIV-1 Group O *env* polypeptide may comprise an immunoreactive portion of the gp41 protein of HIV-1 Group O isolate HAM112.

Among these constructs, those in which the first HIV-1 Group O *env* polypeptide has an amino acid sequence consisting essentially of residues 1 through 520 of the sequence of Figure 1 (SEQ ID NO:61), or a portion thereof, are preferred; more preferred are those in which the first HIV-1 Group O *env* polypeptide has an amino acid sequence consisting essentially of residues 476 through 520 of the sequence of Figure 1 (SEQ ID NO:61). As to the second HIV-1 Group O *env* polypeptide, which may have an amino acid sequence consisting essentially of residues 521 through 873 of the sequence of Figure 1 (SEQ ID NO:61) or a portion thereof and from which a portion of the hydrophobic region of the gp41 protein of HIV-1 Group O isolate HAM112 may optionally be absent, preferred are those constructs in which that second HIV-1 Group O *env* polypeptide has an amino acid sequence consisting essentially of residues 47 through 373 of Figure 9 (SEQ ID NO:52). Even more preferred are those having a second HIV-1 Group O *env* polypeptide with an amino acid sequence consisting essentially of residues 47 through 245 of Figure 7 (SEQ ID NO:48), and

especially those in which the amino acid sequence consists essentially of residues 47 through 215 of Figure 5 (SEQ ID NO:58).

The additional HIV-1 polypeptide in any of these constructs may be a Group O *env* polypeptide; however, it is intended that it may alternatively be an immunogenic polypeptide from any of HIV-1 Groups M or O or HIV-2, including *env*, *gag*, *pol*, reverse transcriptase, and regulatory and other viral components. Preferred in any case are those constructs in which the additional HIV-1 Group O polypeptide comprises an immunoreactive portion of the gp41 protein of HIV-1 Group O isolate HAM112. Also preferred are those wherein the additional HIV-1 Group O polypeptide has an amino acid sequence consisting essentially of residues 521 through 873 of the sequence of Figure 1 (SEQ ID NO:61) or a portion thereof, from which the hydrophobic region of the gp41 protein of HIV-1 Group O isolate HAM112 may optionally be absent. Even more preferred are constructs in which the additional HIV-1 Group O *env* polypeptide has an amino acid sequence consisting essentially of residues 47 through 373 of Figure 9 (SEQ ID NO:52); particularly preferred are those in which the additional HIV-1 Group O *env* polypeptide has an amino acid sequence consisting essentially of residues 47 through 245 of Figure 7 (SEQ ID NO:48), and especially those wherein the additional HIV-1 Group O *env* polypeptide has an amino acid sequence consisting essentially of residues 47 through 215 of Figure 5 (SEQ ID NO:58). Most preferred are constructs having as the additional HIV-1 Group O *env* polypeptide the so-called immunodominant region (IDR) of HIV-1 Group O, which has an amino acid sequence consisting essentially of residues 250 through 281 of Figure 17 (SEQ ID NO:120). Representative of the above constructs are pGO-15CKS and pGO-15PL, as well as any derivatives, variants and analogs thereof.

In still another aspect of the present invention is disclosed an antigen construct comprising a first HIV-2 *env* polypeptide fused to a second HIV-2 *env* polypeptide, and especially one in which the first HIV-2 *env* polypeptide is a gp120 polypeptide and the second HIV-2 *env* polypeptide is a gp36 polypeptide. Preferred among the such constructs are those in which:

(a) the first HIV-2 *env* polypeptide has an amino acid sequence consisting essentially of residues 248 through 307 of the sequence of Figure 11 (SEQ ID NO:55) or a portion thereof; and

(b) the second HIV-2 *env* polypeptide has an amino acid sequence consisting essentially of residues 308 through 466 of the sequence of Figure 11 (SEQ ID NO:55) or a portion thereof.

Representative of the HIV-2 constructs of the invention is pHIV-210 (SEQ ID NO:55), as well as any derivatives, variants and analogs thereof.

An additional aspect of the present invention comprises polynucleotides encoding any of the above antigen construct, which polynucleotide may be operably linked to a control sequence capable of directing expression in a suitable host and/or have a coding sequence

which has been modified to provide a codon bias appropriate to the expression host. Still other aspects of the present invention include expression vectors comprising such polynucleotides and host cells transformed thereby, particularly where the host is *Escherichia coli.*

In a further aspect of the present invention, there is disclosed a method for detecting antibodies to HIV-1 in a test sample comprising the steps of:

(a) combining at least one antigen construct according to the invention with the test sample to form a mixture;

(b) incubating the mixture under conditions suitable for formation of complexes between the antigen and antibodies, if any, which are present in the sample and are immunologically reactive with the antigen; and

(c) detecting the presence of any complexes formed.

In one embodiment of the method, detection of the presence of complexes in step (c) is carried out using an additional antigen construct of the invention to which a signal-generating compound has been attached. In another embodiment, detection is carried out using an additional antigen construct of the invention to which a first member of a specific binding pair is attached, and further using an indicator reagent comprising a second member of the specific binding pair to which is attached a signal-generating compound. A further embodiment provides that detection of the presence of complexes in step (c) is carried out using an antibody directed to the complexes formed in step (b), to which antibody is attached a signal-generating compound. Still another embodiment provides that detection of the presence of complexes in step (c) is carried out using an antibody directed to the complexes formed in step (b) and attached thereto a first member of a specific binding pair; such detection further requires the use of an indicator reagent comprising a second member of the specific binding pair to which is attached a signal-generating compound.

In a final aspect of the present invention are disclosed immunoassay kits for the detection of antibodies to HIV-1, which kits comprise an antigen construct of the invention. Such construct may be used as a capture reagent or an indicator reagent. Alternatively, the antigen construct may be attached to a first member of a specific binding pair, the kit additionally comprising an indicator reagent comprising a second member of the specific binding pair attached to a signal-generating compound.

Brief Description of the Drawings

In the detailed description of the present invention which follows, reference is made to the attached drawings in which:

FIGURE 1 shows the deduced amino acid sequence of the *env* protein from the HIV-1 Group O isolate HAM112 (SEQ ID NO:61).

FIGURE 2 depicts the strategy used to generate synthetic HIV-1 Group O *env* gp120/gp41 gene constructs, wherein the pGO-8 insert = Osyn-5' to Osyn-P3'; pGO-9 insert

= Osyn-5' to Osyn-03'; pGO-11 insert = Osyn-5' to Osyn-M; and wherein H = the hydrophobic region of HIV-1 Group O, deleted as shown.

FIGURES 3A through 3D show a diagrammatic representation of the steps involved in construction of pGO-9PL/DH5α and pGO-9CKS/XL1.

FIGURES 4A through 4G show a diagrammatic representation of the steps involved in construction of pGO-11PL/DH5α and pGO-11CKS/XL1.

FIGURE 5 illustrates the amino acid sequence of the pGO-8PL recombinant protein (SEQ ID NO:58).

FIGURE 6 shows the amino acid sequence of the pGO-8CKS recombinant protein (SEQ ID NO:60).

FIGURE 7 illustrates the amino acid sequence of the pGO-9PL recombinant protein (SEQ ID NO:48).

FIGURE 8 shows the amino acid sequence of the pGO-9CKS recombinant protein (SEQ ID NO:50).

FIGURE 9 illustrates the amino acid sequence of the pGO-11PL recombinant protein (SEQ ID NO:52).

FIGURE 10 shows the amino acid sequence of the pGO-11CKS recombinant protein (SEQ ID NO:54).

FIGURE 11 illustrates the amino acid sequence of the pHIV-210 recombinant protein (SEQ ID NO:55).

FIGURE 12 illustrates the amino acid sequence of the pGM-1CKS recombinant protein (SEQUENCE ID NO: 108).

FIGURE 13 illustrates the amino acid sequence of the pGO-12CKS recombinant protein (SEQ ID NO:91), including an indication of the residues corresponding to the CKS/polylinker, *env* gp120/gp41 from the HIV-1 group M isolate HXB2R, and *env* gp120/gp41 from the HIV-1 group O isolate HAM112.

FIGURE 14 illustrates the amino acid sequence of the pGO-13CKS recombinant protein (SEQ ID NO:93), including an indication of the residues corresponding to the CKS/polylinker, *env* gp120/gp41 from the HIV-1 group M isolate HXB2R, and *env* gp120/gp41 from the HIV-1 group O isolate HAM112.

FIGURE 15 illustrates the amino acid sequence of the pGO-14PL recombinant protein (SEQ ID NO:95), including an indication of the residues corresponding to *env* gp120/gp41 from the HIV-1 group M isolate HXB2R and *env* gp120/gp41 from the HIV-1 group O isolate HAM112.

FIGURE 16 illustrates the amino acid sequence of the pGO-15CKS recombinant protein (SEQ ID NO:97), including an indication of the residues corresponding to the CKS/polylinker, *env* gp120/gp41 from the HIV-1 group O isolate HAM112, a four-amino acid linker, and the second copy of the gp41 IDR from the HAM112 isolate.

FIGURE 17 illustrates the amino acid sequence of the pGO-15PL recombinant protein (SEQ ID NO:120), including an indication of the residues corresponding to *env* gp120/gp41 from the HIV-1 group O isolate HAM112, a four-amino acid linker, and the second copy of the gp41 IDR from the HAM112 isolate.

FIGURES 18-23 show the results obtained in coated-bead immunoassays (described in Example 14, below) testing the reactivity of the Group M antigen pTB319 and Group O recombinant antigens pGO-9CKS, pGO-11PL, pGO-12CKS, pGO-14PL and pGO-15CKS, respectively, with a panel of sera comprising HIVPL-31 (Group M-positive) and sera numbers 14283, 189404, 193Ha, 14791, 267Ha and ESP-1 (all Group O-positive).

Detailed Description of the Invention

In one embodiment of an isolated polypeptide of the present invention, the amino acid sequence of the *env* protein of the HIV-1 Group O isolate HAM112 is shown in Figure 1 (SEQ ID NO:61). In the present context, "isolated" is intended to mean that such polypeptides are relatively purified with respect to other viral or cellular components which normally would be present *in situ*, up to and including a substantially pure preparation of the protein. Such polypeptides can be utilized as assay reagents, for the production of monoclonal or polyclonal antibodies, in the manufacture of vaccines, or otherwise.

Immunoreactive portions, or fragments, of the above polypeptides are also expected to be useful. By "immunoreactive" is meant portions of such length as are capable of eliciting an immune response in a host and/or of reacting with antibodies directed specifically thereto; preferably, such partial polypeptides will be five or more amino acids in length. It should also be noted that the term "portion" as used herein is directed to both terminally truncated sequences and those which are shortened by the removal of an intervening sequence.

The above polypeptides and portions will best be produced by expression of polynucleotides encoding the same. These too permit a degree of variability in their sequence, as for example due to degeneracy of the genetic code, codon bias in favor of the host cell expressing the polypeptide, and conservative amino acid substitutions in the resulting protein. Moreover, it is anticipated that some variation of sequences will occur between -- and possibly even within -- a given HIV-1 isolate or other phylogenetic unit. Consequently, the polypeptides and constructs of the invention include not only those which are identical in sequence to the above sequence but also those which have an amino acid sequence that consist essentially of that reference sequence, where the term "consisting essentially" is meant to embrace variant polypeptides the structural and functional characteristics of which remain substantially the same. Preferably, such variants (or "analogs") will have a sequence homology ("identity") of 80% or more with the reference sequence of Figure 1. In this sense, techniques for determining amino acid sequence "similarity" are well-known in the art. In general, "similarity" means the exact amino acid to amino acid comparison of two or more

polypeptides at the appropriate place, where amino acids are identical or possess similar chemical and/or physical properties such as charge or hydrophobicity. A so-termed "percent similarity" then can be determined between the compared polypeptide sequences. Techniques for determining nucleic acid and amino acid sequence identity also are well known in the art and include determining the nucleotide sequence of the mRNA for that gene (usually via a cDNA intermediate) and determining the amino acid sequence encoded therein, and comparing this to a second amino acid sequence. In general, "identity" refers to an exact nucleotide to nucleotide or amino acid to amino acid correspondence of two polynucleotides or polypeptide sequences, respectively. Two or more polynucleotide sequences can be compared by determining their "percent identity", as can two or more amino acid sequences. The programs available in the Wisconsin Sequence Analysis Package, Version 8 (available from Genetics Computer Group, Madison, WI), for example, the GAP program, are capable of calculating both the identity between two polynucleotides and the identity and similarity between two polypeptide sequences, respectively. Other programs for calculating identity or similarity between sequences are known in the art.

According to another embodiment of the invention, antigen constructs are provided which are suitable for use in the detection of anti-HIV-1 antibodies. As described in greater detail below, such constructs may be prepared by recombinant means, as synthetic peptides, or otherwise; moreover, they may be glycosylated or unglycosylated depending on the manner and/or host cell by which they are made. Consequently, although referred to as if comprising glycoproteins (for example, "a gp120 polypeptide"), the antigen constructs of the invention are intended to include those which are expressed in bacterial hosts such as *E. coli* and are therefore unglycosylated.

It should be noted that the above constructs are fusions of various sequences, that is, the constructs are formed by joining various epitope-containing sequences, as for example by co-expression, ligation or sequential synthesis. Also joined thereto, and optionally included in the constructs of the invention, are other polypeptide sequences such as expression (CKS) polylinkers and other linker sequences. The order of the various polypeptide sequences is not critical; consequently, the polypeptides and their epitopes may be re-arranged as a matter of convenience. Further modifications are also possible, as for example by random mutation or site-directed mutagenesis or even the deletion (removal or omission) of certain regions such as the gp41 hydrophobic region, the absence of which has been found to enhance expression of the remaining polypeptide. In any case, whether nearly the same or substantially changed, polypeptides which undergo these modifications may be said to be "derived" from their respective sources, and the resulting polypeptides may be regarded as "derivatives".

In yet another aspect of the present invention, assay methods are provided which utilize the constructs of the invention in the detection of anti-HIV-1 antibodies in test samples. Such methods permit the direct testing of biological specimens; however, the assay methods may

also be modified to permit the testing of pre-processed specimens such as sera, lysed cells, and extracts or preparations made therefrom (as by concentration, dilution, separation, fixation and/or immobilization). Depending on the desired assay format, the antigen constructs may also be modified for use in such assays, as for example by labeling, immobilization on a solid phase or otherwise, or conjugation to other assay reagents.

Certain terms used herein are intended to have specialized meanings. Unless otherwise stated, the terms below shall have the following meanings:

The term "primer" denotes a specific oligonucleotide sequence complementary to a target nucleotide sequence and used to hybridize to the target nucleotide sequence. It serves as an initiation point for nucleotide polymerization catalyzed by either DNA polymerase, RNA polymerase or reverse transcriptase.

The term "polynucleotide" as used herein means a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. This term refers only to the primary structure of the molecule. Thus, the term includes double- and single-stranded DNA as well as double- and single-stranded RNA. It also includes modifications, such as methylation or capping, and unmodified forms of the polynucleotide.

"Encoded by" refers to a nucleic acid sequence which codes for a polypeptide sequence. Also encompassed are polypeptide sequences which are immunologically identifiable with a polypeptide encoded by the sequence. Thus, a "polypeptide," "protein," or "amino acid" sequence as claimed herein may have at least 60% similarity, more preferably at least about 70% similarity, and most preferably about 80% similarity to a particular polypeptide or amino acid sequence specified below.

The terms "recombinant polypeptide" or "recombinant protein", used interchangeably herein, describe a polypeptide which by virtue of its origin or manipulation is not associated with all or a portion of the polypeptide with which it is associated in nature and/or is linked to a polypeptide other than that to which it is linked in nature. A recombinant or encoded polypeptide or protein is not necessarily translated from a designated nucleic acid sequence. It also may be generated in any manner, including chemical synthesis or expression of a recombinant expression system.

"Polypeptide" and "protein" are used interchangeably herein and indicate a molecular chain of amino acids linked through covalent and/or noncovalent bonds. The terms do not refer to a specific length of the product. Thus, peptides, oligopeptides and proteins are included within the definition of polypeptide. The terms include post-expression modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the like. In addition, protein fragments, analogs, mutated or variant proteins, fusion proteins and the like are included within the meaning of polypeptide.

A "fragment" of a specified polypeptide refers to an amino acid sequence which comprises at least about 3-5 amino acids, more preferably at least about 8-10 amino acids, and even more preferably at least about 15-20 amino acids, derived from the specified polypeptide.

The term "synthetic peptide" as used herein means a polymeric form of amino acids of any length, which may be chemically synthesized by methods well-known to those skilled in the art. These synthetic peptides are useful in various applications.

"Purified polypeptide" means a polypeptide of interest or fragment thereof which is essentially free, that is, contains less than about 50%, preferably less than about 70%, and more preferably, less than about 90% of cellular components with which the polypeptide of interest is naturally associated. Methods for purifying are known in the art.

The term "isolated" means that the material is removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or DNA or polypeptide, which is separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotide could be part of a vector and/or such polynucleotide or polypeptide could be part of a composition, and still be isolated in that the vector or composition is not part of its natural environment.

"Recombinant host cells," "host cells," "cells," "cell lines," "cell cultures," and other such terms denoting microorganisms or higher eukaryotic cell lines cultured as unicellular entities refer to cells which can be, or have been, used as recipients for recombinant vector or other transferred DNA, and include the original progeny of the original cell which has been transfected.

As used herein "replicon" means any genetic element, such as a plasmid, a chromosome or a virus, that behaves as an autonomous unit of polynucleotide replication within a cell.

A "vector" is a replicon to which another polynucleotide segment is attached, such as to bring about the replication and/or expression of the attached segment.

The term "control sequence" refers to polynucleotide sequences which are necessary to effect the expression of coding sequences to which they are ligated. The nature of such control sequences differs depending upon the host organism. In prokaryotes, such control sequences generally include promoter, ribosomal binding site and terminators; in eukaryotes, such control sequences generally include promoters, terminators and, in some instances, enhancers. The term "control sequence" thus is intended to include at a minimum all components whose presence is necessary for expression, and also may include additional components whose presence is advantageous, for example, leader sequences.

"Operably linked" refers to a situation wherein the components described are in a relationship permitting them to function in their intended manner. Thus, for example, a control

sequence "operably linked" to a coding sequence is ligated in such a manner that expression of the coding sequence is achieved under conditions compatible with the control sequences.

A "coding sequence" is a polynucleotide sequence which is transcribed into mRNA and translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by and include a translation start codon at the 5' -terminus and one or more translation stop codons at the 3' -terminus. A coding sequence can include, but is not limited to, mRNA, cDNA, and recombinant polynucleotide sequences.

The term "immunologically identifiable with/as" refers to the presence of epitope(s) and polypeptide(s) which also are present in and are unique to the designated polypeptide(s). Immunological identity may be determined by antibody binding and/or competition in binding. These techniques are known to the skilled artisan and also are described herein. The uniqueness of an epitope also can be determined by computer searches of known data banks, such as GenBank, for the polynucleotide sequences which encode the epitope, and by amino acid sequence comparisons with other known proteins.

As used herein, "epitope" means an antigenic determinant of a polypeptide. Conceivably, an epitope can comprise three amino acids in a spatial conformation which is unique to the epitope. Generally, an epitope consists of at least five such amino acids, and more usually, it consists of at least eight to ten amino acids. Methods of examining spatial conformation are known in the art and include, for example, x-ray crystallography and two-dimensional nuclear magnetic resonance.

A "conformational epitope" is an epitope that is comprised of specific juxtaposition of amino acids in an immunologically recognizable structure, such amino acids being present on the same polypeptide in a contiguous or non-contiguous order or present on different polypeptides.

A polypeptide is "immunologically reactive" with an antibody when it binds to an antibody due to antibody recognition of a specific epitope contained within the polypeptide. Immunological reactivity may be determined by antibody binding, more particularly by the kinetics of antibody binding, and/or by competition in binding using as competitor(s) a known polypeptide(s) containing an epitope against which the antibody is directed. The methods for determining whether a polypeptide is immunologically reactive with an antibody are known in the art.

The term "transformation" refers to the insertion of an exogenous polynucleotide into a host cell, irrespective of the method used for the insertion. For example, direct uptake, transduction or f-mating are included. The exogenous polynucleotide may be maintained as a non-integrated vector, for example, a plasmid, or alternatively, may be integrated into the host genome.

The term "test sample" refers to a component of an individual's body which is the source of the analyte (such as, antibodies of interest or antigens of interest). These components are well known in the art. These test samples include biological samples which can be tested by the methods of the present invention described herein and include human and animal body fluids such as whole blood, serum, plasma, cerebrospinal fluid, urine, lymph fluids, and various external secretions of the respiratory, intestinal and genitorurinary tracts, tears, saliva, milk, white blood cells, myelomas and the like; biological fluids such as cell culture supernatants; fixed tissue specimens; and fixed cell specimens.

"Purified product" refers to a preparation of the product which has been isolated from the cellular constituents with which the product is normally associated, and from other types of cells which may be present in the sample of interest.

The present invention provides assays which utilize specific binding members. A "specific binding member," as used herein, is a member of a specific binding pair. That is, two different molecules where one of the molecules through chemical or physical means specifically binds to the second molecule. Therefore, in addition to antigen and antibody specific binding pairs of common immunoassays, other specific binding pairs can include biotin and avidin, carbohydrates and lectins, complementary nucleotide sequences, effector and receptor molecules, cofactors and enzymes, enzyme inhibitors and enzymes, and the like. Furthermore, specific binding pairs can include members that are analogs of the original specific binding members, for example, an analyte-analog. Immunoreactive specific binding members include antigens, antigen fragments, antibodies and antibody fragments, both monoclonal and polyclonal, and complexes thereof, including those formed by recombinant DNA molecules.

A "capture reagent," as used herein, refers to an unlabeled specific binding member which is specific either for the analyte as in a sandwich assay, for the indicator reagent or analyte as in a competitive assay, or for an ancillary specific binding member, which itself is specific for the analyte, as in an indirect assay. The capture reagent can be directly or indirectly bound to a solid phase material before the performance of the assay or during the performance of the assay, thereby enabling the separation of immobilized complexes from the test sample.

The "indicator reagent" comprises a "signal-generating compound" ("label") which is capable of generating and generates a measurable signal detectable by external means, conjugated ("attached") to a specific binding member. "Specific binding member" as used herein means a member of a specific binding pair. That is, two different molecules where one of the molecules through chemical or physical means specifically binds to the second molecule. In addition to being an antibody member of a specific binding pair, the indicator reagent also can be a member of any specific binding pair, including either hapten-anti-hapten systems such as biotin or anti-biotin, avidin or biotin, a carbohydrate or a lectin, a complementary nucleotide sequence, an effector or a receptor molecule, an enzyme cofactor and an enzyme, an enzyme

inhibitor or an enzyme, and the like. An immunoreactive specific binding member can be an antibody, an antigen, or an antibody/antigen complex that is capable of binding either to polypeptide of interest as in a sandwich assay, to the capture reagent as in a competitive assay, or to the ancillary specific binding member as in an indirect assay.

The various "signal-generating compounds" (labels) contemplated include chromogens, catalysts such as enzymes, luminescent compounds such as fluorescein and rhodamine, chemiluminescent compounds such as dioxetanes, acridiniums, phenanthridiniums and luminol, radioactive elements, and direct visual labels. Examples of enzymes include alkaline phosphatase, horseradish peroxidase, beta-galactosidase, and the like. The selection of a particular label is not critical, but it will be capable of producing a signal either by itself or in conjunction with one or more additional substances.

"Solid phases" ("solid supports") are known to those in the art and include the walls of wells of a reaction tray, test tubes, polystyrene beads, magnetic beads, nitrocellulose strips, membranes, microparticles such as latex particles, sheep (or other animal) red blood cells, and Duracytes® (red blood cells "fixed" by pyruvic aldehyde and formaldehyde, available from Abbott Laboratories, Abbott Park, IL) and others. The "solid phase" is not critical and can be selected by one skilled in the art. Thus, latex particles, microparticles, magnetic or non-magnetic beads, membranes, plastic tubes, walls of microtiter wells, glass or silicon chips, sheep (or other suitable animal's) red blood cells and Duracytes® are all suitable examples. Suitable methods for immobilizing peptides on solid phases include ionic, hydrophobic, covalent interactions and the like. A "solid phase", as used herein, refers to any material which is insoluble, or can be made insoluble by a subsequent reaction. The solid phase can be chosen for its intrinsic ability to attract and immobilize the capture reagent. Alternatively, the solid phase can retain an additional receptor which has the ability to attract and immobilize the capture reagent. The additional receptor can include a charged substance that is oppositely charged with respect to the capture reagent itself or to a charged substance conjugated to the capture reagent. As yet another alternative, the receptor molecule can be any specific binding member which is immobilized upon (attached to) the solid phase and which has the ability to immobilize the capture reagent through a specific binding reaction. The receptor molecule enables the indirect binding of the capture reagent to a solid phase material before the performance of the assay or during the performance of the assay. The solid phase thus can be a plastic, derivatized plastic, magnetic or non-magnetic metal, glass or silicon surface of a test tube, microtiter well, sheet, bead, microparticle, chip, sheep (or other suitable animal's) red blood cells, Duracytes® and other configurations known to those of ordinary skill in the art.

It is contemplated and within the scope of the present invention that the solid phase also can comprise any suitable porous material with sufficient porosity to allow access by detection antibodies and a suitable surface affinity to bind antigens. Microporous structure generally are preferred, but materials with gel structure in the hydrated state may be used as well. Such

useful solid supports include but are not limited to nitrocellulose and nylon. It is contemplated that such porous solid supports described herein preferably are in the form of sheets of thickness from about 0.01 to 0.5 mm, preferably about 0.1 mm. The pore size may vary within wide limits, and preferably is from about 0.025 to 15 microns, especially from about 0.15 to 15 microns. The surface of such supports may be activated by chemical processes which cause covalent linkage of the antigen or antibody to the support. The irreversible binding of the antigen or antibody is obtained, however, in general, by adsorption on the porous material by poorly understood hydrophobic forces. Other suitable solid supports are known in the art.

The present invention provides polynucleotide sequences derived from human immunodeficiency viruses of interest and polypeptides encoded thereby. The polynucleotide(s) may be in the form of mRNA or DNA. Polynucleotides in the form of DNA, cDNA, genomic DNA, and synthetic DNA are within the scope of the present invention. The DNA may be double-stranded or single-stranded, and if single stranded may be the coding (sense) strand or non-coding (anti-sense) strand. The coding sequence which encodes the polypeptide may be identical to the coding sequence provided herein or may be a different coding sequence which coding sequence, as a result of the redundancy or degeneracy of the genetic code, encodes the same polypeptide as the DNA provided herein.

This polynucleotide may include only the coding sequence for the polypeptide, or the coding sequence for the polypeptide and additional coding sequence such as a leader or secretory sequence or a proprotein sequence, or the coding sequence for the polypeptide (and optionally additional coding sequence) and non-coding sequence, such as a non-coding sequence 5' and/or 3' of the coding sequence for the polypeptide.

In addition, the invention includes variant polynucleotides containing modifications such as polynucleotide deletions, substitutions or additions; and any polypeptide modification resulting from the variant polynucleotide sequence. A polynucleotide of the present invention also may have a coding sequence which is a naturally-occurring variant of the coding sequence provided herein.

In addition, the coding sequence for the polypeptide may be fused in the same reading frame to a polynucleotide sequence which aids in expression and secretion of a polypeptide from a host cell, for example, a leader sequence which functions as a secretory sequence for controlling transport of a polypeptide from the cell. The polypeptide having a leader sequence is a preprotein and may have the leader sequence cleaved by the host cell to form the form of the polypeptide. The polynucleotides may also encode for a proprotein which is the protein plus additional 5' amino acid residues. A protein having a prosequence is a proprotein and may in some cases be an inactive form of the protein. Once the prosequence is cleaved an active protein remains. Thus, the polynucleotide of the present invention may encode for a

protein, or for a protein having a prosequence or for a protein having both a presequence (leader sequence) and a prosequence.

The polynucleotides of the present invention may also have the coding sequence fused in frame to a marker sequence which allows for purification of the polypeptide of the present invention. The marker sequence may be a hexa-histidine tag supplied by a pQE-9 vector to provide for purification of the polypeptide fused to the marker in the case of a bacterial host, or, for example, the marker sequence may be a hemagglutinin (HA) tag when a mammalian host, e.g. COS-7 cells, is used. The HA tag corresponds to an epitope derived from the influenza hemagglutinin protein. See, for example, I. Wilson et al., *Cell* 37:767 (1984).

The present invention further relates to HIV-1 polypeptides which have the deduced amino acid sequence as provided herein, as well as fragments, analogs and derivatives of such polypeptides. The polypeptides of the present invention may be recombinant polypeptides, natural purified polypeptides or synthetic polypeptides. The fragment, derivative or analog of such a polypeptide may be one in which one or more of the amino acid residues is substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code; or it may be one in which one or more of the amino acid residues includes a substituent group; or it may be one in which the polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol); or it may be one in which the additional amino acids are fused to the polypeptide, such as a leader or secretory sequence or a sequence which is employed for purification of the polypeptide or a proprotein sequence. Such fragments, derivatives and analogs are within the scope of the present invention. The polypeptides and polynucleotides of the present invention are preferably provided in an isolated form, and preferably purified.

Thus, a polypeptide of the present invention may have an amino acid sequence that is identical to that of the naturally-occurring polypeptide or that is different by minor variations due to one or more amino acid substitutions. The variation may be a "conservative change" typically in the range of about 1 to 5 amino acids, wherein the substituted amino acid has similar structural or chemical properties, e.g., replacement of leucine with isoleucine or threonine with serine. In contrast, variations may include nonconservative changes, e.g., replacement of a glycine with a tryptophan. Similar minor variations may also include amino acid deletions or insertions, or both. Guidance in determining which and how many amino acid residues may be substituted, inserted or deleted without changing biological or immunological activity may be found using computer programs well known in the art, for example, DNASTAR software (DNASTAR Inc., Madison WI).

The recombinant polypeptides of the present invention can be produced not only as demonstrated below, but also according to a number of alternative methods and using a variety of host cells and expression vectors. Host cells are genetically engineered (transduced or

transformed or transfected) with the vectors of this invention which may be a cloning vector or an expression vector. The vector may be in the form of a plasmid, a viral particle, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying HIV-derived genes. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

The polynucleotides of the present invention may be employed for producing a polypeptide by recombinant techniques. Thus, the polynucleotide sequence may be included in any one of a variety of expression vehicles, in particular vectors or plasmids for expressing a polypeptide. Such vectors include chromosomal, nonchromosomal and synthetic DNA sequences, e.g., derivatives of SV40; bacterial plasmids; phage DNA; yeast plasmids; vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus, and pseudorabies. However, any other plasmid or vector may be used so long as it is replicable and viable in the host.

The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into appropriate restriction endonuclease sites by procedures known in the art. Such procedures and others are deemed to be within the scope of those skilled in the art. The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. Representative examples of such promoters include but are not limited to LTR or SV40 promoter, the *E. coli* lac or trp, the phage lambda P sub L promoter and other promoters known to control expression of genes in prokaryotic or eukaryotic cells or their viruses. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression. In addition, the expression vectors preferably contain a gene to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E. coli*.

The vector containing the appropriate DNA sequence as hereinabove described, as well as an appropriate promoter or control sequence, may be employed to transform an appropriate host to permit the host to express the protein. As representative examples of appropriate hosts, there may be mentioned: bacterial cells, such as *E. coli*, *Salmonella typhimurium*; *Streptomyces sp.*; fungal cells, such as yeast; insect cells such as Drosophila and Sf9; animal cells such as chinese hamster ovary (CHO), COS or Bowes melanoma; plant cells, etc. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings provided herein.

More particularly, the present invention also includes recombinant constructs comprising one or more of the sequences as broadly described above. The constructs comprise

a vector, such as a plasmid or viral vector, into which a sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available. The following vectors are provided by way of example. Bacterial: pINCY (Incyte Pharmaceuticals Inc., Palo Alto, CA), pSPORT1 (Life Technologies, Gaithersburg, MD), pQE70, pQE60, pQE-9 (Qiagen) pBs, phagescript, psiX174, pBluescript SK, pBsKS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia). However, any other plasmid or vector may be used as long as it is replicable and viable in the host.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, SP6, T7, gpt, lambda P sub R, P sub L and trp. Eukaryotic promoters include cytomegalovirus (CMV) immediate early, herpes simplex virus (HSV) thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

The host cell used herein can be a higher eukaryotic cell, such as a mammalian cell, or a lower eukaryotic cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-Dextran mediated transfection, or electroporation (L. Davis et al., "Basic Methods in Molecular Biology", 2nd edition, Appleton and Lang, Paramount Publishing, East Norwalk, CT [1994]).

The constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Alternatively, the polypeptides of the invention can be synthetically produced by conventional peptide synthesizers.

Proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems also can be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, (Cold Spring Harbor, N.Y., 1989), which is hereby incorporated by reference.

Transcription of a DNA encoding the polypeptides of the present invention by higher eukaryotes is increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Examples include the SV40 enhancer on the late side of the replication origin (bp

100 to 270), a cytomegalovirus early promoter enhancer, a polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and the *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), alpha factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a routine matter of choice.

Useful expression vectors for bacterial use comprise a selectable marker and bacterial origin of replication derived from plasmids comprising genetic elements of the well-known cloning vector pBR322 (ATCC 37017). Other vectors include but are not limited to PKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM1 (Promega Biotec, Madison, WI). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is derepressed by appropriate means (e.g., temperature shift or chemical induction), and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents; such methods are well-known to the ordinary artisan.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey

kidney fibroblasts described by Gluzman, *Cell* 23:175 (1981), and other cell lines capable of expressing a compatible vector, such as the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, 5' flanking nontranscribed sequences, and selectable markers such as the neomycin phosphotransferase gene. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Representative, useful vectors include pRc/CMV and pcDNA3 (available from Invitrogen, San Diego, CA).

The HIV-derived polypeptides are recovered and purified from recombinant cell cultures by known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, hydroxyapatite chromatography or lectin chromatography. It is preferred to have low concentrations (approximately 0.1-5 mM) of calcium ion present during purification (Price et al., *J. Biol. Chem.* 244:917 [1969]). Protein refolding steps can be used, as necessary, in completing configuration of the protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

The polypeptides of the present invention may be naturally purified products expressed from a high expressing cell line, or a product of chemical synthetic procedures, or produced by recombinant techniques from a prokaryotic or eukaryotic host (for example, by bacterial, yeast, higher plant, insect and mammalian cells in culture). Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated with mammalian or other eukaryotic carbohydrates or may be non-glycosylated. The polypeptides of the invention may also include an initial methionine amino acid residue.

The present invention further includes modified versions of the recombinant polypeptide to preclude glycosylation while allowing expression of a reduced carbohydrate form of the protein in yeast, insect or mammalian expression systems. Known methods for inactivating gylcosylation sites include, but are not limited to, those presented in U.S. patent 5,071,972 and EP 276,846, which are incorporated herein by reference.

Other variants included in the present invention include those obtained by removal removal of sequences encoding cystein residues, thereby preventing formation of incorrect intramolecular disulfide bridges which decrease biological activity of the protein product. The constructs of the present invention also may be prepared by removal of the site of proteolytic processing, allowing expression in systems which contain a problematic protease, for example the KEX2 protease in yeast. Known methods for removing such protease sites include but are not limited to one method for removing KEX2 sites presented in EP212,914.

The present invention includes the above peptides in the form of oligomers, dimers, trimers and higher order oligomers. Oligomers may be formed by several means including but not limited to disulfide bonds between peptides, non-covalent interactions between peptides, and poly-ethylene-glycol linkages between peptides.

The fusion of the above peptides to peptide linkers or peptides that are capable of promoting oligomers is also encompassed in this invention. Such peptides include but are not limited to leucine zippers and antibody derived peptides, such as is described in Landschulz et al., *Science* 240:1759 (1988); Hollenbaugh and Aruffo, "Construction of Immunoglobin Fusion Proteins", in *Current Protocols in Immunology, Supplement 4*, pgs 10.19.1-10.19.11 (1992) John Wiley and sons, New York, NY.

The starting plasmids can be constructed from available plasmids in accord with published, known procedures. In addition, equivalent plasmids to those described are known in the art and will be apparent to the ordinarily skilled artisan.

Once homogeneous cultures of recombinant cells are obtained, large quantities of recombinantly produced protein can be recovered from the conditioned medium and analyzed using chromatographic methods well known in the art. An alternative method for the production of large amounts of secreted protein involves the transformation of mammalian embryos and the recovery of the recombinant protein from milk produced by transgenic cows, goats, sheep, etc. Polypeptides and closely related molecules may be expressed recombinantly in such a way as to facilitate protein purification. One approach involves expression of a chimeric protein which includes one or more additional polypeptide domains not naturally present on human polypeptides. Such purification-facilitating domains include, but are not limited to, metal-chelating peptides such as histidine-tryptophan domains that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp, Seattle, WA). The inclusion of a cleavable linker sequence such as Factor XA or enterokinase from Invitrogen (San Diego, CA) between the polypeptide sequence and the purification domain may be useful for recovering the polypeptide.

It is also contemplated and within the scope of the present invention that the above recombinant antigens will be used in a variety of immunoassay formats, including but not limited to direct and indirect assays. The means for adapting the antigens to such various formats -- as by conjugation to labels or macromolecules, or immobilization on suitable support surfaces -- are well-understood and should be familiar to those skilled in the art.

For example, the polypeptides including their fragments or derivatives or analogs thereof of the present invention, or cells expressing them, can be used for the detection of antibodies to HIV (as well as an immunogen to produce antibodies). These antibodies can be, for example, polyclonal or monoclonal antibodies, chimeric, single chain and humanized

antibodies, as well as Fab fragments, or the product of an Fab expression library. Various procedures known in the art may be used for the production of such antibodies and fragments.

Further, antibodies generated against a polypeptide corresponding to a sequence of the present invention can be obtained by direct injection of the polypeptide into an animal or by administering the polypeptide to an animal such as a mouse, rabbit, goat or human. A mouse, rabbit or goat is preferred. The antibody so obtained then will bind the polypeptide itself. In this manner, even a sequence encoding only a fragment of the polypeptide can be used to generate antibodies that bind the native polypeptide. Such antibodies can then be used to isolate the polypeptide from test samples such as tissue suspected of containing that polypeptide. For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique as described by Kohler and Milstein, *Nature* 256:495-497 (1975), the trioma technique, the human B-cell hybridoma technique as described by Kozbor et al, *Immun. Today* 4:72 (1983), and the EBV-hybridoma technique to produce human monoclonal antibodies as described by Cole et al., in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc, New York, NY, pp. 77-96 (1985). Techniques described for the production of single chain antibodies can be adapted to produce single chain antibodies to immunogenic polypeptide products of this invention. See, for example, U.S. Pat. No. 4,946,778, which is incorporated herein by reference.

Various assay formats may utilize such antibodies, including "sandwich" immunoassays and probe assays. For example, the monoclonal antibodies or fragment as described above can be employed in various assay systems to determine the presence, if any, of HIV-derived polypeptide in a test sample. For example, in a first assay format, a polyclonal or monoclonal antibody or fragment thereof, or a combination of these antibodies, which has been coated on a solid phase, is contacted with a test sample, to form a first mixture. This first mixture is incubated for a time and under conditions sufficient to form antigen/antibody complexes. Then, an indicator reagent comprising a monoclonal or a polyclonal antibody or a fragment thereof, or a combination of these antibodies, to which a signal generating compound has been attached, is contacted with the antigen/antibody complexes to form a second mixture. This second mixture then is incubated for a time and under conditions sufficient to form antibody/antigen/antibody complexes. The presence of an HIV-derived polypeptide antigen present in the test sample and captured on the solid phase, if any, is determined by detecting the measurable signal generated by the signal generating compound. The amount of HIV-derived polypeptide antigen present in the test sample is proportional to the signal generated.

Or, a polyclonal or monoclonal HIV-derived polypeptide antibody or fragment thereof, or a combination of these antibodies which is bound to a solid support, the test sample and an indicator reagent comprising a monoclonal or polyclonal antibody or fragments thereof, which specifically binds to HIV-derived polypeptide antigen, or a combination of these antibodies to

which a signal generating compound is attached, are contacted to form a mixture. This mixture is incubated for a time and under conditions sufficient to form antibody/antigen/antibody complexes. The presence, if any, of HIV-derived polypeptide present in the test sample and captured on the solid phase is determined by detecting the measurable signal generated by the signal generating compound. The amount of HIV-derived polypeptide proteins present in the test sample is proportional to the signal generated.

In another assay format, one or a combination of at least two monoclonal antibodies can be employed as a competitive probe for the detection of antibodies to HIV-derived polypeptide protein. For example, HIV-derived polypeptide proteins such as the recombinant antigens disclosed herein, either alone or in combination, are coated on a solid phase. A test sample suspected of containing antibody to HIV-derived polypeptide antigen then is incubated with an indicator reagent comprising a signal generating compound and at least one monoclonal antibody for a time and under conditions sufficient to form antigen/antibody complexes of either the test sample and indicator reagent bound to the solid phase or the indicator reagent bound to the solid phase. The reduction in binding of the monoclonal antibody to the solid phase can be quantitatively measured.

In yet another detection method, each of the monoclonal or polyclonal antibodies can be employed in the detection of HIV-derived polypeptide antigens in fixed tissue sections, as well as fixed cells by immunohistochemical analysis. Cytochemical analysis wherein these antibodies are labeled directly (with, for example, fluorescein, colloidal gold, horseradish peroxidase, alkaline phosphatase, etc.) or are labeled by using secondary labeled anti-species antibodies (with various labels as exemplified herein) may be used to track the histopathology of disease.

In addition, these monoclonal antibodies can be bound to matrices similar to CNBr-activated Sepharose and used for the affinity purification of specific HIV-derived polypeptide proteins from cell cultures or biological tissues such as to purify recombinant and native HIV-derived polypeptide antigens and proteins.

Monoclonal antibodies can also be used for the generation of chimeric antibodies for therapeutic use, or other similar applications.

The monoclonal antibodies or fragments thereof can be provided individually to detect HIV-derived polypeptide antigens. Combinations of the monoclonal antibodies (and fragments thereof) also may be used together as components in a mixture or "cocktail" of at least one HIV-derived polypeptide antibodywith antibodies to other HIV-derived polypeptide regions, each having different binding specificities. Thus, this cocktail can include monoclonal antibodies which are directed to HIV-derived polypeptide proteins of HIV and other monoclonal antibodies to other antigenic determinants of the HIV-derived polypeptide genome.

The polyclonal antibody or fragment thereof which can be used in the assay formats should specifically bind to an HIV-derived polypeptide region or other HIV-derived

polypeptide proteins used in the assay. The polyclonal antibody used preferably is of mammalian origin; human, goat, rabbit or sheep anti-HIV-derived polypeptide polyclonal antibody can be used. Most preferably, the polyclonal antibody is rabbit polyclonal anti-HIV-derived polypeptide antibody. The polyclonal antibodies used in the assays can be used either alone or as a cocktail of polyclonal antibodies. Since the cocktails used in the assay formats are comprised of either monoclonal antibodies or polyclonal antibodies having different HIV-derived polypeptide specificity, they would be useful for diagnosis, evaluation and prognosis of HIV-derived polypeptide condition, as well as for studying HIV-derived polypeptide protein differentiation and specificity.

It is contemplated and within the scope of the present invention that HIV-derived polypeptides may be detectable in assays by use of recombinant antigens as well as by use of synthetic peptides or purified peptides, which contain amino acid sequences of HIV-derived polypeptides. It also is within the scope of the present invention that different synthetic, recombinant or purified peptides identifying different epitopes of each such HIV-derived polypeptide can be used in combination in an assay to diagnose, evaluate, or prognosticate the HIV disease condition. In this case, these peptides can be coated onto one solid phase, or each separate peptide may be coated on separate solid phases, such as microparticles, and then combined to form a mixture of peptides which can be later used in assays. Furthermore, it is contemplated that multiple peptides which define epitopes from different polypeptides may be used in combination to make a diagnosis, evaluation, or prognosis of HIV disease. Peptides coated on solid phases or labeled with detectable labels are then allowed to compete with peptides from a patient sample for a limited amount of antibody. A reduction in binding of the synthetic, recombinant, or purified peptides to the antibody (or antibodies) is an indication of the presence of HIV-secreted polypeptides in the patient sample which in turn indicates the presence of HIV gene in the patient. Such variations of assay formats are known to those of ordinary skill in the art and are discussed herein below.

In another assay format, the presence of antigens and/or antibodies to HIV-derived polypeptides can be detected in a simultaneous assay, as follows. A test sample is simultaneously contacted with a capture reagent of a first analyte, wherein said capture reagent comprises a first binding member specific for a first analyte attached to a solid phase and a capture reagent for a second analyte, wherein said capture reagent comprises a first binding member for a second analyte attached to a second solid phase, to thereby form a mixture. This mixture is incubated for a time and under conditions sufficient to form capture reagent/first analyte and capture reagent/second analyte complexes. These so-formed complexes then are contacted with an indicator reagent comprising a member of a binding pair specific for the first analyte labeled with a signal generating compound and an indicator reagent comprising a member of a binding pair specific for the second analyte labeled with a signal generating compound to form a second mixture. This second mixture is incubated for a time and under

conditions sufficient to form capture reagent/first analyte/indicator reagent complexes and capture reagent/second analyte/indicator reagent complexes. The presence of one or more analytes is determined by detecting a signal generated in connection with the complexes formed on either or both solid phases as an indication of the presence of one or more analytes in the test sample. In this assay format, recombinant antigens may be utilized as well as monoclonal antibodies produced therefrom. Such assay systems are described in greater detail in EP Publication No. 0473065.

In yet other assay formats, the polypeptides disclosed herein may be utilized to detect the presence of antibodies specific for HIV-derived polypeptides in test samples. For example, a test sample is incubated with a solid phase to which at least one recombinant protein has been attached. These are reacted for a time and under conditions sufficient to form antigen/antibody complexes. Following incubation, the antigen/antibody complex is detected. Indicator reagents may be used to facilitate detection, depending upon the assay system chosen. In another assay format, a test sample is contacted with a solid phase to which a recombinant protein produced as described herein is attached and also is contacted with a monoclonal or polyclonal antibody specific for the protein, which preferably has been labeled with an indicator reagent. After incubation for a time and under conditions sufficient for antibody/antigen complexes to form, the solid phase is separated from the free phase, and the label is detected in either the solid or free phase as an indication of the presence of HIV-derived polypeptide antibody. Other assay formats utilizing the recombinant antigens disclosed herein are contemplated. These include contacting a test sample with a solid phase to which at least one antigen from a first source has been attached, incubating the solid phase and test sample for a time and under conditions sufficient to form antigen/antibody complexes, and then contacting the solid phase with a labeled antigen, which antigen is derived from the same source or, alternatively, a second source different from the first source. For example, a recombinant protein derived from a first source such as *E. coli* is used as a capture antigen on a solid phase, a test sample is added to the so-prepared solid phase, and a recombinant protein derived from a different source (i.e., non-*E. coli*) is utilized as a part of an indicator reagent. Likewise, combinations of a recombinant antigen on a solid phase and synthetic peptide in the indicator phase also are possible. Any assay format which utilizes an antigen specific for HIV-derived polypeptide from a first source as the capture antigen and an antigen specific for HIV-derived polypeptide from a second source are contemplated. Thus, various combinations of recombinant antigens, as well as the use of synthetic peptides, purified proteins, and the like, are within the scope of this invention. Assays such as this and others are described in U.S. Patent No. 5,254,458, which enjoys common ownership and is incorporated herein by reference.

Other embodiments which utilize various other solid phases also are contemplated and are within the scope of this invention. For example, ion capture procedures for immobilizing

an immobilizable reaction complex with a negatively charged polymer (described in EP publication 0326100 and EP publication No. 0406473), can be employed according to the present invention to effect a fast solution-phase immunochemical reaction. An immobilizable immune complex is separated from the rest of the reaction mixture by ionic interactions between the negatively charged poly-anion/immune complex and the previously treated, positively charged porous matrix and detected by using various signal generating systems previously described, including those described in chemiluminescent signal measurements as described in EPO Publication No. 0 273,115.

Also, the methods of the present invention can be adapted for use in systems which utilize microparticle technology including in automated and semi-automated systems wherein the solid phase comprises a microparticle (magnetic or non-magnetic). Such systems include those described in published EPO applications Nos. EP 0 425 633 and EP 0 424 634, respectively.

The use of scanning probe microscopy (SPM) for immunoassays also is a technology to which the monoclonal antibodies of the present invention are easily adaptable. In scanning probe microscopy, in particular in atomic force microscopy, the capture phase, for example, at least one of the monoclonal antibodies of the invention, is adhered to a solid phase and a scanning probe microscope is utilized to detect antigen/antibody complexes which may be present on the surface of the solid phase. The use of scanning tunneling microscopy eliminates the need for labels which normally must be utilized in many immunoassay systems to detect antigen/antibody complexes. The use of SPM to monitor specific binding reactions can occur in many ways. In one embodiment, one member of a specific binding partner (analyte specific substance which is the monoclonal antibody of the invention) is attached to a surface suitable for scanning. The attachment of the analyte specific substance may be by adsorption to a test piece which comprises a solid phase of a plastic or metal surface, following methods known to those of ordinary skill in the art. Or, covalent attachment of a specific binding partner (analyte specific substance) to a test piece which test piece comprises a solid phase of derivatized plastic, metal, silicon, or glass may be utilized. Covalent attachment methods are known to those skilled in the art and include a variety of means to irreversibly link specific binding partners to the test piece. If the test piece is silicon or glass, the surface must be activated prior to attaching the specific binding partner. Also, polyelectrolyte interactions may be used to immobilize a specific binding partner on a surface of a test piece by using techniques and chemistries. The preferred method of attachment is by covalent means. Following attachment of a specific binding member, the surface may be further treated with materials such as serum, proteins, or other blocking agents to minimize non-specific binding. The surface also may be scanned either at the site of manufacture or point of use to verify its suitability for assay purposes. The scanning process is not anticipated to alter the specific binding properties of the test piece.

While the present invention discloses the preference for the use of solid phases, it is contemplated that the reagents such as antibodies, proteins and peptides of the present invention can be utilized in non-solid phase assay systems. These assay systems are known to those skilled in the art, and are considered to be within the scope of the present invention.

The present invention will be better understood in connection with the following examples, which are meant to illustrate, but not to limit, the spirit and scope of the invention.

Example 1
Cloning Procedures

Oligonucleotides for gene construction and sequencing were synthesized at Abbott Laboratories, Synthetic Genetics (San Diego, CA) or Oligo Etc. (Wilsonville, CA). All polymerase chain reaction (PCR) reagents, including AmpliTaq DNA polymerase and UlTma DNA polymerase, were purchased from Perkin-Elmer Corporation (Foster City, CA) and used according to the manufacturer's specifications unless otherwise indicated. PCR amplifications were performed on a GeneAmp 9600 thermal cycler (Perkin-Elmer). Unless indicated otherwise, restriction enzymes were purchased from New England BioLabs (Beverly, MA) and digests were performed as recommended by the manufacturer. DNA fragments used for cloning were isolated on agarose (Life Technologies, Gaithersburg, MD) gels, unless otherwise indicated.

Desired fragments were excised and the DNA was extracted with a QIAEX II gel extraction kit or the QIAquick gel extraction kit (Qiagen Inc., Chatsworth, CA) as recommended by the manufacturer. DNA was resuspended in H_20 or TE [1 mM ethylenediaminetetraacetic acid (EDTA; pH 8.0; BRL Life Technologies), 10 mM tris(hydroxymethyl)aminomethane-hydrochloride (Tris-HCl; pH 8.0; BRL Life Technologies)]. Ligations were performed using a Stratagene DNA ligation kit (Stratagene Cloning Systems, La Jolla, CA) as recommended by the manufacturer. Ligations were incubated at 16°C overnight.

Bacterial transformations were performed using MAX EFFICIENCY DH5α competent cells (BRL Life Technologies) or Epicurian Coli XL1-Blue supercompetent cells (Stratagene Cloning Systems) following the manufacturer's protocols. Unless indicated otherwise, transformations and bacterial restreaks were plated on LB agar (Lennox) plates with 150 µg/ml ampicillin (M1090; MicroDiagnostics, Lombard, IL) or on LB agar + ampicillin plates supplemented with glucose to a final concentration of 20mM, as noted. All bacterial incubations (plates and overnight cultures) were conducted overnight (~16 hours) at 37°C.

Screening of transformants to identify desired clones was accomplished by sequencing of miniprep DNA and/or by colony PCR. Miniprep DNA was prepared with a Qiagen Tip 20 Plasmid Prep Kit or a Qiagen QIAwell 8 Plasmid Prep Kit following the manufacturer's specifications, unless otherwise indicated. For colony PCR screening, individual colonies were picked from transformation plates and transferred into a well in a sterile flat-bottom 96-well plate (Costar, Cambridge, MA) containing 100 µl sterile H_2O. One-third of the volume was transferred to a second plate and stored at 4°C. The original 96-well plate was microwaved for 5 minutes to disrupt the cells. 1 µl volume then was transferred to a PCR tube as template. 9 µl of a PCR master mix containing 1 µl 10X PCR buffer, 1 µl 2 mM dNTPs, 1 µl (10 pmol) sense primer, 1 µl (10 pmol) anti-sense primer, 0.08 µl AmpliTaq DNA polymerase (0.4 units), and 4.2 µl H_2O was added to the PCR tube. Reactions were generally amplified for 20-25 cycles of 94°C for 30 seconds, 50-60°C (depending on primer annealing temperatures) for 30 seconds and 72°C for 60 seconds. Primers were dependent on the insert and cycle conditions were modified based on primer annealing temperatures and the length of the expected product. After cycling, approximately 1/3 of the reaction volume was loaded on an agarose gel for analysis. Colonies containing desired clones were propagated from the transfer plate.

Unless otherwise indicated, DNA sequencing was performed on an automated ABI Model 373A Stretch Sequencer (Perkin Elmer). Sequencing reactions were set up with reagents from a FS TACS Dye Term Ready Reaction Kit (Perkin Elmer) and 250-500 ng plasmid DNA according to the manufacturer's specifications. Reactions were processed on Centri-Sep columns (Princeton Separations, Adelphia, N.J.) prior to loading on the Sequencer. Sequence data was analyzed using Sequencher 3.0 (Gene Codes Corporation, Ann Arbor, MI) and GeneWorks 2.45 (Oxford Molecular Group, Inc., Campbell, CA).

Example 2

Determination of the *env* Sequence of the HIV-1 Group O Isolate HAM112

Viral RNA was extracted from culture supernatants of human peripheral blood mononuclear cells infected with the HIV-1 Group O isolate designated HAM112 (H. Hampl et al., *Infection* 23:369-370 [1995]) using a QIAamp Blood Kit (Qiagen) and the manufacturer's recommended procedure. RNA was eluted in a 50 µl volume of nuclease-free water (5Prime-3Prime, Inc., Boulder, CO) and stored at -70°C. The strategy for obtaining the *env* region sequence involved cDNA synthesis and PCR (nested) amplification of four overlapping *env* gene fragments. The amplified products were sequenced directly on an automated ABI Model

373A Stretch Sequencer. Amplification reactions were carried out with GeneAmp RNA PCR and GeneAmp PCR Kits (Perkin Elmer) as outlined by the manufacturer. Oligonucleotide primer positions correspond to the HIV-1 ANT70 *env* sequence (G. Myers et al., eds., *supra*). The primers env10R [nucleotide (nt) 791-772; SEQ ID NO:62], env15R (nt 1592-1574; SEQ ID NO:63), env22R (nt 2321-2302; SEQ ID NO:64), env26R (nt 250-232 3' of *env*; SEQ ID NO:65) were used for cDNA synthesis of fragments 1-4, respectively. Reverse transcription reactions were incubated at 42°C for 30 minutes then at 99°C for 5 minutes. First-round PCR amplifications consisted of 30 cycles of 95°C for 30 seconds, 52°C for 30 seconds, and 72°C for 1 minute using the primer combinations: env1F (nt 184-166 5' of *env*; SEQ ID NO:66) and env10R (SEQ ID NO:62), env7F (nt 564-586; SEQ ID NO:67) and env15R (SEQ ID NO:63), env12F (nt 1289-1308; SEQ ID NO:68) and env22R (SEQ ID NO:64), env19F (nt 2020-2040; SEQ ID NO:69) and env26R (SEQ ID NO:65) for fragments 1 through 4, respectively. For the second round of amplification (nested PCR), 5 µl of the respective first-round PCR reactions was used as template along with the primer combinations env2F (nt 37-15 5' of *env*; SEQ ID NO:70) and env9R (nt 740-721; SEQ ID NO:71), env8F (nt 631-650; SEQ ID NO:72) and env14R (nt 1437-1416; SEQ ID NO:73), env13F (nt 1333-1354; SEQ ID NO:74) and env21R (nt 2282-2265; SEQ ID NO:75), env20F (nt 2122-2141; SEQ ID NO:76) and env25R (nt 111-94 3' of *env*; SEQ ID NO:77) for fragments 1 through 4, respectively. Second-round amplification conditions were identical to those used for the first round. Fragments were agarose gel-purified and extracted with a Qiagen QIAEX II Gel Extraction Kit. Fragments were sequenced directly with the primers used for nested PCR along with primers env4F (SEQ ID NO:78) and env5R (SEQ ID NO:79) for fragment 1; primers env10F (SEQ ID NO:80), env11F (SEQ ID NO:81), env11R (SEQ ID NO:82), env12F (SEQ ID NO:68), and AG1 (SEQ ID NO:87) for fragment 2; primers env15F (SEQ ID NO:83) and env19R (SEQ ID NO:84) for fragment 3; primers env22F (SEQ ID NO:85) and env24R (SEQ ID NO:86) for fragment 4. The deduced amino acid sequence of *env* from the HIV-1 Group O isolate HAM112 (SEQ ID NO:61) is presented in FIGURE 1.

Example 3

Construction of Synthetic HIV-1 Group O *env* gp120 /gp41 Genes

FIGURE 2 depicts the strategy used to generate synthetic HIV-1 Group O *env* gp120/gp41 gene constructs. The *env* gp120/gp41 sequences were based on the HIV-1 Group O isolate HAM112 (SEQ ID NO:61). Determination of the *env* sequence of HAM112 is outlined in Example 2, hereinabove. Oligonucleotides were designed that encode the C-terminal 45 amino acids of the *env* gp120 and 327 amino acids of *env* gp41 (nucleotide #1 is the first base of the first codon of gp120 in the synthetic gene). The synthetic gene has a 26 amino acid deletion (nucleotides 643 through 720), relative to the native HAM112 gp41, that

encompasses a highly hydrophobic (H) region (transmembrane region) of gp41. Thus, the full-length synthetic gp41 gene constructed is 327 amino acids.

In the synthetic oligonucleotides, the native HIV-1 codons were altered to conform to *E. coli* codon bias in an effort to increase expression levels of the recombinant protein in *E. coli*. See, for example, M. Gouy and C. Gautier, *Nucleic Acids Research* 10:7055 (1982); H. Grosjean and W. Fiers, *Gene* 18:199 (1982); J. Watson et al. (eds.), *Molecular Biology of the Gene*, 4th Ed., Benjamin Kumming Publishing Co., pp.440 (1987). The gene construction strategy involved synthesis of a series of overlapping oligonucleotides with complementary ends (Osyn-A through Osyn-L, depicted as A through L). When annealed, the ends served as primers for the extension of the complementary strand.

The fragments then were amplified by PCR. This process ("PCR knitting" of oligonucleotides) was reiterated to progressively enlarge the gene fragment. Oligonucleotide Osyn-5' was designed for cloning into the PL vector pKRR826. The expression vector, pKRR826, is a modified form of the lambda pL promoter vector pSDKR816, described in U.S. Serial No. 08/314,570, incorporated herein by reference. pKRR826 is a high copy number derivative of pBR322 that contains the temperature sensitive cI repressor gene (Benard et al., *Gene* 5:59 [1979]). However, pKRR826 lacks the translational terminator rrnBt1 and has the lambda pL and lambda pR promoters in the reverse orientation, relative to pSDKR816. The polylinker region of pKRR826 contains Eco RI and Bam HI restriction enzyme sites but lacks an ATG start codon. Optimal expression is obtained when the 5' end of the gene insert (including an N-terminal methionine) is cloned into the EcoRI site. Osyn-5' was designed to contain an Eco RI restriction site for cloning and an ATG codon (methionine) to provide for proper translational initiation of the recombinant proteins. The anti-sense oligonucleotides Osyn-O3' (SEQ ID NO:15), Osyn-P3' (SEQ ID NO:16), and Osyn-M (M) (SEQ ID NO:14) each contain two sequential translational termination codons (TAA,TAG) and a Bam HI restriction site. When outside primers Osyn-5' (SEQ ID NO:11) and Osyn-M (M) (SEQ ID NO:14) were used, a full-length gp41 (327 amino acids) gene was synthesized (pGO-11PL; SEQ ID NO:52). Outside oligonucleotides Osyn-5' (SEQ ID NO:11) and Osyn-O3' (SEQ ID NO:15) resulted in a truncated gp41 product of 199 amino acids (pGO-9PL; SEQ ID NO:48). Alternatively, outside oligonucleotides Osyn-5' (SEQ ID NO:11) and Osyn-P3' (SEQ ID NO:16) resulted in a truncated gp41 product 169 amino acids in length (pGO-8PL; SEQ ID NO:58).

The synthetic genes also were expressed as CMP-KDO synthetase (CKS) fusion proteins. PCR-mediated transfer of the synthetic genes from pKRR826 into pJO200 (described in U.S. Serial No. 572,822, and incorporated herein by reference) was accomplished with an alternative outside sense oligonucleotide PCR primer (5' end), Osyn-5'CKS (SEQ ID NO:25). Osyn-5'CKS contained an Eco RI restriction site and resulted in the in-frame fusion of the synthetic gene insert to CKS in the expression vector pJO200. The 3'

outside primers (antisense) Osyn-M (SEQ ID NO:14), Osyn-O3' (SEQ ID NO:15) and Osyn-P3' (SEQ ID NO:16) were used in combination with Osyn-5'CKS (SEQ ID NO:25) to generate pGO-11CKS (SEQ ID NO:54), pGO-9CKS (SEQ ID NO:50), and pGO-8 CKS (SEQ ID NO:60), respectively. These steps are detailed hereinbelow.

A. PCR Knitting of Synthetic Oligonucleotides.

Three PCR reactions (100 µl volume) were set up as follows:

(1) Reaction 1B: AmpliTaq DNA polymerase (2.5U) and 1X buffer, along with 40µM of each dNTP (dATP, dCTP, dGTP, and dTTP), 25 pmol each of oligonucleotides Osyn-A (SEQ ID NO:3) and Osyn-D (SEQ ID NO:5), and 0.25 pmol each of oligonucleotides Osyn-B (SEQ ID NO:17) and Osyn-C (SEQ ID NO:4);

(2) Reaction 2A: UlTma DNA Polymerase (3U) and 1X buffer along with 1.5mM $MgCl_2$, 40µM of each dNTP, 25pmol each of oligonucleotides Osyn-E (SEQ ID NO:6) and Osyn-H (SEQ ID NO:9), and 0.25 pmol each of oligonucleotides Osyn-F (SEQ ID NO:7) and Osyn-G (SEQ ID NO:8); and

(3) Reaction 3A: UlTma DNA Polymerase (3U) and 1X buffer along with 1.5mM $MgCl_2$, 40µM of each dNTP, 25pmol each of oligonucleotides Osyn-I (SEQ ID NO:10) and Osyn-L (SEQ ID NO:13), and 0.25 pmol each of oligonucleotides Osyn-J (SEQ ID NO:18) and Osyn-K (SEQ ID NO:12).

Amplifications consisted of 20 cycles of 97°C for 30 seconds, 52°C for 30 seconds and 72°C for 60 seconds. Reactions were then incubated at 72°C for 7 minutes and held at 4°C. PCR-derived products 1B, 2A and 3B were gel isolated on a 1% agarose gel.

B. PCR Knitting of PCR Products From Reaction 1B and Reaction 2A.

A PCR reaction was set up with UlTma DNA Polymerase (3U) and 1X buffer along with 1.5mM $MgCl_2$, 40µM of each dNTP, 24.4pmol of oligonucleotide Osyn-5' (SEQ ID NO:11), 25 pmol of oligonucleotide Osyn-P3' (SEQ ID NO:16), and ~10 ng each of gel-isolated 1B and 2A products from Example 3, Section 1A, hereinabove. Cycling conditions were the same as in Example 3, Section 1A. A second round of amplification was used to generate more of the desired product. This was performed by making an UlTma mix as described hereinabove (100 µl reaction volume) with 49 pmol Osyn-5' (SEQ ID NO:11), 50 pmol Osyn-P3' (SEQ ID NO:16) and 5 µl of the PCR product from the first round as template. These reactions were incubated at 94°C for 90 seconds, and then cycled as above (Section 3A). The Osyn-5'/Osyn-P3' PCR product was gel-isolated as described hereinabove.

C. Cloning of the Osyn-5'-Osyn-P3' PCR Product.

The Osyn-5'-Osyn-P3' PCR product was digested with the restriction endonucleases Eco RI + Bam HI and ligated into the vector pKRR826 (described hereinabove) that had been digested with Eco RI + Bam HI and gel-isolated. The ligation product was used to transform DH5α competent cells. The desired clone was identified by colony PCR using oligonucleotides pKRREcoRI Forward (SEQ ID NO:38) and pKRRBamHI Reverse (SEQ ID NO:39). Miniprep DNA was prepared from an overnight culture of pGO-8 candidate clone A2 and the Osyn-5'-Osyn-P3' plasmid insert was sequenced with the oligonucleotide primers pKRREcoRI Forward (SEQ ID NO:38), pKRRBamHI Reverse (SEQ ID NO:39), 41sy-1 (SEQ ID NO:44), and 41sy-2 (SEQ ID NO:41).

D. Modification of pGO-8 Candidate Clone A2.

A 100 µl volume PCR reaction was set up with UlTma DNA Polymerase (3U) and 1X buffer, along with 1.5mM $MgCl_2$, 40µM of each dNTP, 50pmol of oligonucleotides Osyn-5'-repair (SEQ ID NO:24), 50 pmol Osyn-P3' (SEQ ID NO:16), and ~1 ng of pGO-8 candidate clone A2 miniprep DNA as template (obtained from the reactions set forth hereinabove). The reaction was incubated at 94°C for 90 seconds, and then amplified with 20 cycles of 94°C for 30 seconds, 50°C for 30 seconds and 72°C for 60 seconds. The Osyn-5'-repair/Osyn-P3' PCR product then was gel isolated and digested with Eco RI + Bam HI. The digested product was ligated into Eco RI + Bam HI digested pKRR826 vector. The ligation product was used to transform DH5α competent cells. The desired clone was identified by colony PCR using oligonucleotides pKRREcoRI Forward (SEQ ID NO:38) and pKRRBamHI Reverse (SEQ ID NO:39). An overnight culture of pGO-8 candidate clone 6 was set up and a miniprep DNA was prepared. The Osyn-5'repair/Osyn-P3' plasmid insert was sequenced with the oligonucleotide primers pKRREcoRI Forward (SEQ ID NO:38), pKRRBamHI Reverse (SEQ ID NO:39), 41sy-1 (SEQ ID NO:44), and 41sy-2 (SEQ ID NO:41). Based on the sequencing results, pGO-8 candidate clone #6 was designated pGO-8PL/DHSα. SEQ ID NO:57 presents the nucleotide sequence of the coding region. FIGURE 5 presents the amino acid sequence of the pGO-8PL recombinant protein (SEQ ID NO:58). The pGO-8PL recombinant protein consists of a N-terminal methionine, 45 amino acids of *env* gp120 (HIV-1 Group O, HAM112 isolate), and 169 amino acids of *env* gp41 (HIV-1 Group O, HAM112 isolate).

E. Construction of pGO-8CKS/XL1.

pGO-8CKS/XL1 (SEQ ID NO:59 presents the nucleotide sequence of the coding region) encodes the recombinant protein pGO-8CKS. FIGURE 6 presents the amino acid sequence of pGO-8CKS (SEQ ID NO:60). This protein consists of 246 amino acids of CKS/

polylinker, 45 amino acids of *env* gp120 (HIV-1 Group O, HAM112 isolate), and 169 amino acids of *env* gp41 (HIV-1 Group O, HAM112 isolate). The construction of pGO-8CKS/XL1 was accomplished as follows.

A PCR reaction (100 µl volume) was set up with UlTma DNA Polymerase (3U) and 1X buffer along with 1.5mM $MgCl_2$, 40µM of each dNTP, 50pmol of Osyn-5'CKS (SEQ ID NO:25), 50 pmol Osyn-P3' (SEQ ID NO:16), and 1 ng pGO-8PL clone #6 miniprep DNA. The reaction was incubated at 94°C for 90 seconds then amplified with 25 cycles of 94°C for 30 seconds; 55°C for 30 seconds; 72°C for 90 seconds. Then, the Osyn-5'CKS/Osyn-P3' PCR product was gel isolated. EcoR I + Bam HI digested the Osyn-5'CKS/Osyn-P3' PCR product and the vector pJO200. The digested pJO200 vector was gel isolated and ligated to digested Osyn-5'CKS/Osyn-P3' PCR product. XL1-Blue supercompetent cells were transformed with the ligation and plated on LB + ampicillin plates supplemented with 20 mM glucose. Colonies were restreaked for isolation on the same type of plates. An overnight culture of clone pGO-8CKS/XL1 was grown in LB broth + 100µg/ml carbenicillin (Sigma Chemical Co.)+ 20 mM glucose (Sigma Chemical Co.). Frozen stocks (0.5 ml overnight culture + 0.5 ml glycerol) were made and DNA was prepared for sequence analysis. The following oligonucleotides were used as sequencing primers: CKS-1 (SEQ ID NO:30), CKS-2 (SEQ ID NO:31), CKS-3 (SEQ ID NO:32), CKS-4 (SEQ ID NO:33), 43461 (SEQ ID NO:2), 43285 (SEQ ID NO:1), 41sy-1B (SEQ ID NO:29), 41sy-2B (SEQ ID NO:34), CKS176.1 (SEQ ID NO:19), and CKS3583 (SEQ ID NO:20).

F. Construction of pGO-9PL/DH5α.

FIGURES 3A through 3D and show a diagrammatic representation of the steps involved in construction of pGO-9PL/DH5α. pGO-9PL/DH5α encodes the recombinant protein pGO-9PL. SEQ ID NO:47 present the nucleotide sequence of the coding region of pGO-9PL/DH5α. FIGURE 7 illustrates the amino acid sequence of the pGO-9PL recombinant protein (SEQ ID NO:48). This protein consists of an N-terminal methionine, 45 amino acids of *env* gp120 (HIV-1 Group O, HAM112 isolate), and 199 amino acids of *env* gp41 (HIV-1 Group O, HAM112 isolate). Construction of pGO-9PL/DH5α was accomplished as follows.

Step 1: A 100 µl PCR reaction was set up with UlTma DNA Polymerase (3U) and 1X buffer, along with 1.5mM $MgCl_2$, 40µM of each dNTP, 50pmol of Osyn-5' (SEQ ID NO:11), 50 pmol of Osyn-H (SEQ ID NO:9), and ~2 ng of pGO-8 candidate clone 6 miniprep DNA (obtained from Example 3, Section D hereinabove) as template. The reaction was incubated at 94°C for 120 seconds, and then amplified with 8 cycles of 94°C for 30 seconds, 55°C for 30 seconds and 72°C for 60 seconds.

Step 2: A 100 µl PCR reaction was set up with UlTma DNA Polymerase (3U) and 1X buffer along with 1.5mM $MgCl_2$, 40µM of each dNTP, 50pmol of Osyn-5' (SEQ ID NO:11), 50 pmol Osyn-O3' (SEQ ID NO:15), and 10 µl of the PCR reaction from step 1 as template. The reaction was incubated at 94°C for 120 seconds then amplified with 18 cycles of 94°C for 30 seconds, 55°C for 30 seconds, 72°C for 60 seconds, followed by incubation at 72°C for 5 minutes.

The Osyn-5'/Osyn-O3' PCR product (2A/2B) then was gel-isolated and digested with Eco RI + Bam HI. The digested product was ligated into Eco RI + Bam HI digested pKRR826 vector. The ligation product next was used to transform DH5α competent cells. An overnight culture of pGO-9PL candidate clone 3 was set up and a miniprep DNA was prepared. The Osyn-5'/Osyn-O3' plasmid insert was sequenced with the following oligonucleotides as primers: pKRREcoR1 Forward (SEQ ID NO:38), pKRRBamHI Reverse (SEQ ID NO:39), 41sy-1C (SEQ ID NO:40), 41sy-2 (SEQ ID NO:41), 41sy-3 (SEQ ID NO:42) and 41sy-4 (SEQ ID NO:23). pGO-9PL clone #3 then was restreaked for isolation. An isolated colony was picked, an overnight culture of it was grown, and a frozen stock (0.5ml glycerol + 0.5ml overnight culture) was made. The stock was stored at -80°C. The sequence was confirmed using the primers indicated hereinabove, and this clone was designated as pGO-9PL/DH5α (SEQ ID NO:47 presents the nucleotide sequence of the coding region, and SEQ ID NO:48 presents the amino acid sequence of coding region). pGO-9PL/DH5α was restreaked, an overnight culture was grown, and a miniprep DNA was prepared (this prep was designated as H5).

G. Construction of pGO-9CKS/XL1

FIGURE 3A through 3D show a diagrammatic representation of the steps involved in construction of pGO-9CKS/XL1. pGO-9CKS/XL1 encodes the recombinant protein pGO-9CKS. FIGURE 8 presents the amino sequence of the pGO-9CKS recombinant protein (SEQ ID NO:50). This protein consists of 246 amino acids of CKS and polylinker followed by 45 amino acids of *env* gp120 (HIV-1 Group O, HAM112 isolate), and 199 amino acids of *env* gp41 (HIV-1 Group O, HAM112 isolate). The construction of pGO-9CKS/XL1 was accomplished as follows.

Two PCR reactions (100 µl volume) were set up with UlTma DNA Polymerase (3U) and 1X buffer, along with 1.5mM $MgCl_2$, 40µM of each dNTP, 50pmol of Osyn-5'CKS (SEQ ID NO:25), 50 pmol Osyn-O3' (SEQ ID NO:15) and 1 ng pGO-9PL candidate clone 3 miniprep DNA (obtained from Example 3, Section F, hereinabove). Each reaction was incubated at 94°C for 120 seconds, then amplified with 24 cycles of 94°C for 30 seconds, 55°C for 30 seconds, 72°C for 120 seconds, followed by incubation at 72°C for 5 minutes. The

Osyn-5'CKS/Osyn-O3' PCR product then was gel isolated. The Osyn-5'CKS/Osyn-O3' PCR product and the vector pJO200 was digested with EcoR I + Bam HI. The digested pJO200 vector was gel isolated and ligated to the digested Osyn-5'CKS/Osyn-O3' PCR product. XL1-Blue supercompetent cells were transformed with the ligation and plated on LB + ampicillin plates supplemented with 20 mM glucose. Colonies were restreaked for isolation on the same type of plates. An overnight culture of clone pGO-9CKS candidate clone 4 was grown in LB broth + 100 mg/ml carbenicillin (Sigma Chemical Co.)+ 20 mM glucose (Sigma Chemical Co.). Made frozen stocks (0.5 ml overnight culture + 0.5 ml glycerol) and prepared DNA for sequence analysis. The following oligonucleotides were used as sequencing primers: CKS-1 (SEQ ID NO:30), CKS-2 (SEQ ID NO:31), CKS-3 (SEQ ID NO:32), CKS-4 (SEQ ID NO:33), 43461 (SEQ ID NO:2), 43285 (SEQ ID NO:1), 41sy-1B (SEQ ID NO:29), 41sy-2B (SEQ ID NO:34), 41sy-3B (SEQ ID NO:35), CKS176.1 (SEQ ID NO:19), CKS3583 (SEQ ID NO:20), and pTB-S8 (SEQ ID NO:28). Clone pGO-9CKS candidate clone 4 was designated as pGO-9CKS/XL1 (SEQ ID NO:49 presents the nucleotide sequence of coding region, and SEQ ID NO:50 presents the amino acid sequence of coding region).

H. Construction of Osyn I-M Fragment.

The Osyn-O-M fragment was constructed as follows. A 100 µl PCR reaction was set up using AmpliTaq DNA Polymerase (2.5U), 1X buffer, 50 µM of each dNTP, 50pmol I-PCR (SEQ ID NO:26), 50 pmol Osyn-M (SEQ ID NO:14) and 10 ng of gel-isolated PCR fragment 3A (Example 3, section A, hereinabove). The reaction was incubated at 95°C for 105 seconds, and then it was amplified with 15 cycles of 95°C for 30 seconds, 55°C for 30 seconds, 72°C for 60 seconds, and then it was held at 72°C for 7 minutes. The product, designated as Osyn I-M, was gel-isolated and cloned into the PCR II vector (TA Cloning Kit ; Invitrogen, San Diego, CA) following the manufacturer's recommended procedure. The resulting ligation product was used to transform DH5α competent cells. Plasmid miniprep DNA was generated from an overnight culture of clone IM-6, and the gene insert was sequenced with oligonucleotides 56759 (SEQUENCE ID NO: 45) and 55848 (SEQ ID NO:46).

I. Synthesis and Knitting of PCR Fragments I/6R and IM-6F.

These procedures were performed as follows.

Step 1: The following PCR reactions (100 µl volume) were set up: (a) I/6R with AmpliTaq DNA Polymerase (2.5U), 1X buffer, 50 µM of each dNTP, 50pmol I-PCR (SEQ ID NO:26), 50 pmol IM-6R (SEQ ID NO:22) and 281 ng of clone IM-6 (obtained from Example 3, Section H) as template; (b) 6F/M with AmpliTaq DNA Polymerase (2.5U), 1X

buffer, 50 μM of each dNTP, 50pmol IM-6F (SEQ ID NO:21), 50 pmol M-PCR (SEQ ID NO:27) and 281 ng of clone IM-6 (obtained from Example 3, Section H) as template.

The reactions were incubated at 95°C for 105 seconds, and then amplified with 20 cycles of 94°C for 15 seconds, 60°C for 30 seconds, 72°C for 60 seconds, then incubated at 72°C for 7 minutes. The PCR products I/6R and 6F/M next were gel isolated following the procedures as described hereinabove.

Step 2: A PCR reaction (100 μl volume) was set up with UlTma DNA Polymerase (3U) and 1X buffer along with 1.5mM $MgCl_2$, 40μM of each dNTP, 50pmol of I-PCR (SEQ ID NO:26), 50 pmol M-PCR (SEQ ID NO:27), ~50 ng I/6R, and ~20ng 6F/M. The reaction was incubated at 95°C for 105 seconds, and then it was amplified with 20 cycles of 94°C for 15 seconds, 55°C for 30 seconds, 72°C for 60 seconds, followed by incubation at 72°C for 7 minutes. The PCR product was processed on a Centri-sep column (Princeton Separations) following the manufacturer's instructions.

J. Construction of pGO-11PL/DH5α.

FIGURES 4A through 4F show a diagrammatic representation of the steps involved in construction of pGO-11PL/DH5α. pGO-11PL/ DH5α encodes the recombinant protein pGO-11PL. FIGURE 9 presents the amino acid sequence of the pGO-11PL recombinant protein (SEQ ID NO:52). This protein consists of an N-terminal methionine, 45 amino acids of *env* gp120 (HIV-1 Group O, HAM112 isolate), and 327 amino acids of *env* gp41 (HIV-1 Group O, HAM112 isolate). pGO-11PL/ DH5α was constructed as follows.

The final PCR product from Example 3, Section I and pGO-9PL vector (miniprep H5 from Example 3, section F) were digested sequentially with Age I and Bam HI. The digested pGO-9PL was then treated with calf intestinal alkaline phosphatase (BRL Life Technologies) for 15 minutes at 37°C, phenol/chloroform extracted, and precipitated with NaOAc and EtOH. The vector (pGO-9PL) was subsequently gel-isolated. The digested pGO-9PL and the digested PCR product were ligated, and the ligation product was used to transform DH5α competent cells. Colonies were restreaked for isolation. Clone pGO11-4 then was identified and restreaked for isolation. An overnight culture of pGO11-4 was prepared in order to generate frozen stocks and perform miniprep DNA for sequencing. Clone pGO11-4 was sequenced with the following oligonucleotide primers: pKRREcoR1 Forward (SEQ ID NO:38), pKRRBamHI Reverse (SEQ ID NO:39), 41sy-1C (SEQ ID NO:40), 41sy-2 (SEQ ID NO:41), 41sy-3 (SEQUENCE ID NO: 42), 41sy-4 (SEQ ID NO:23), 41sy-5B (SEQ ID NO:43), 41sy-5C (SEQ ID NO:36) and 41sy-6B (SEQ ID NO:37). Based on the sequencing results, this clone was designated as pGO-11PL/DH5α (SEQ ID NO:51 presents the nucleotide

sequence of the coding region, and SEQ ID NO:52 presents the amino acid sequence of coding region).

K. Construction of pGO-11CKS/XL1.

FIGURES 4A through 4G show a diagrammatic representation of the steps involved in construction of pGO-11CKS/XL1. pGO-11CKS/XL1 encodes the recombinant protein pGO-11CKS. FIGURE 10 shows the amino sequence of the pGO-11CKS recombinant protein (SEQ ID NO:54). This protein consists of 246 amino acids of CKS and polylinker followed by 45 amino acids of *env* gp120 (HIV-1 Group O, HAM112 isolate), and 327 amino acids of *env* gp41 (HIV-1 Group O, HAM112 isolate). pGO-11CKS/XL1 was constructed as follows.

A PCR reaction (100 µl volume) was set up with UlTma DNA Polymerase (3U) and 1X buffer along with 1.5mM $MgCl_2$, 40µM of each dNTP, 50pmol of Osyn-5'CKS (SEQ ID NO:25), 50 pmol Osyn-M (SEQ ID NO:14), and 1 ng pG011-4 (obtained from Example 3, Section J) as template. The reaction was incubated at 94°C for 105 seconds, and then amplified with 20 cycles of 94°C for 30 seconds, 55°C for 30 seconds, 72°C for 120 seconds, followed by incubation at 72°C for 7 minutes. The Osyn-5'CKS/Osyn-M PCR product was gel isolated. Next, the Osyn-5'CKS/Osyn-M PCR product and the vector pJO200 were EcoR I + Bam HI digested. The digested pJO200 vector was gel isolated. Overnight (16°C) ligations were set up with the digested PCR product. XL1-Blue supercompetent cells were transformed with the ligation and plated on LB + ampicillin plates supplemented with 20 mM glucose. Colonies were restreaked for isolation on the same plates. An overnight culture (LB medium + 100µg/ml carbenicillin + 20 mM glucose) of clone pGO-11CKS clone candidate 2 then was set up. Frozen stocks (0.5 ml 80% glycerol + 0.5 ml overnight culture) were made as well as miniprep DNA for sequencing. The following oligonucleotides were used as primers for sequence analysis: CKS-1 (SEQ ID NO:30), CKS-2 (SEQ ID NO:31), CKS-3 (SEQ ID NO:32), CKS-4 (SEQ ID NO:33), 43461 (SEQ ID NO:2), 43285 (SEQ ID NO:1), 41sy-1B (SEQ ID NO:29), 41sy-2B (SEQ ID NO:34), 41sy-3B (SEQ ID NO:35), 41sy-4 (SEQ ID NO:23), 41sy-5C (SEQ ID NO:36), 41sy-6B (SEQ ID NO:37), CKS176.1 (SEQ ID NO:19), CKS3583 (SEQ ID NO:20), and pTB-S8 (SEQ ID NO:28). pGO-11CKS clone #2 was designated as pGO-11CKS/XL1. SEQ ID NO:53 presents the nucleotide sequence of the coding region of pGO-11CKS/XL1, and SEQ ID NO:54 presents the amino acid sequence of the coding region of pGO-11CKS/XL1.

Example 4
Construction of pHIV210/XL1-Blue

FIGURE 11 presents the amino acid sequence of the pHIV-210 recombinant protein (SEQ ID NO:55). This protein consists of 247 amino acids of CKS/linker sequences, 60 amino acids from *env* gp120 (#432-491; HIV-2 isolate D194.10), and 159 amino acids of *env* gp36 (#492-650; HIV-2 isolate D194.10). The construction of pHIV210/XL1-Blue was accomplished as follows.

The genomic DNA of HIV-2 isolate D194.10 [H. Kuhnel et al., *Nucleic Acids Research* 18: 6142 (1990)] was cloned into the EMBL3 lambda cloning vector. See H. Kuhnel et al., *Proc. Nat'l. Acad. Sci. USA* 86: 2383-2387 (1989), and H. Kuhnel et al., *Nucleic Acids Research* 18: 6142 (1990), incorporated herein by reference. The lambda clone containing D194.10 (lambda A10) was obtained from Diagen Corporation (Düsseldorf, Germany). A PCR reaction (100 µl volume) was set up using AmpliTaq DNA polymerase (3.75 units), 200µM each dATP, dCTP, dGTP, and dTTP, 0.5 µg primer 3634 (SEQ ID NO:88; annealing to positions 7437-7455 on the HIV-2 isolate D194.10 (EMBL accession #X52223), 0.5 µg primer 3636 (SEQ ID NO:89, annealing to positions 8095-8077), 1X PCR buffer, and 5 µl of the lambda A10 DNA diluted 1:50. The reaction was incubated 5 minutes at 94°C then amplified with 35 cycles of 94°C for 1 minute, 45°C for 1 minute, 72°C for 2 minutes; followed by an incubation at 72°C for 5 minutes. The PCR reaction was extracted with phenol/chloroform (Boehringer Mannheim Corporation, Indianapolis, IN) and the DNA was ethanol (AAPER Alcohol & Chemical Company, Shelbyville, KY) precipitated. The DNA was digested with EcoRI + Bam HI and gel purified on an 1.5% agarose gel (SeaKem GTG agarose, FMC Corporation, Rockland, Maine). The purified product was ligated into EcoRI + Bam HI digested pJO200 vector using 800 units of T4 DNA ligase (New England BioLabs). XL1-Blue supercompetent cells (Stratagene) were transformed with 2 µl of the ligation as outlined by the manufacturer and plated on LB plates supplemented with ampicillin (Sigma Chemical Company). Overnight cultures were established by inoculating single colonies into Superbroth II media (GIBCO BRL, Grand Island, NY) supplemented with 50 µg/ml ampicillin (Sigma) and 20mM glucose (Sigma). Frozen stocks were established by adding 0.3 ml of 80% glycerol to 0.7 ml of overnight. After mixing stocks were stored at -70°C. Miniprep DNA was prepared from the overnight cultures using the alkaline lysis method followed by PEG precipitation. Sequence reactions were performed with a 7-deaza-dGTP Reagent Kit with Sequenase Version 2.0 (United States Biochemical Corporation, Cleveland, OH) as outlined by the manufacturer. Reactions were run on 6% acrylamide gels (GIBCO BRL Gel-Mix 6) using the IBI gel apparatus as recommended by the manufacturer. Based on sequencing results, pHIV-210 clone #7 was designated as pHIV-210. The amino acid sequence of the pHIV-210 coding region is presented as SEQ ID NO:55.

Example 5

Growth And Induction of *E. coli* Strains with HIV-1 Group O Recombinant gp41 Antigen Construct

Overnight seed cultures of pGO-9CKS/XL1 and pGO-11CKS/XL1 were prepared in 500 ml sterile Excell Terrific Broth (available from Sigma Chemical Corp., St. Louis Mo.) supplemented with 100 µg/ml sodium ampicillin, and placed in a shaking orbital incubator at 32°C or 37°C. One hundred milliliter (100 µl) inocula from seed cultures were transferred to flasks containing 1 liter sterile Excell Terrific Broth supplemented with 100 µg/ml sodium ampicillin. Cultures were incubated at 37°C until the culture(s) reached mid-logarithmic growth and then induced with 1 mM ITPG (isopropylthiogalactoside) for 3 hours at 37°C. (In the case of PL vector constructs, cultures were incubated at 32°C until the culture(s) reached mid-logarithmic growth and then induced for 3 hours by shifting the temperature of the culture(s) to 42°C.) After the induction period, cells were pelleted by centrifugation and harvested following standard procedures. Pelleted cells were stored at -70°C until further processed.

Example 6

Isolation and Solubilization of HIV-1 Group O Recombinant gp41 Antigen Produced as Insoluble Inclusion Bodies in *E. coli*

Frozen cells obtained from Example 5 were resuspended by homogenization in cold lysis buffer comprising 50 mM Tris pH 8, 10 mM Na EDTA , 150 mM NaCl, 8% (w/v) sucrose, 5% Triton X-100® (v/v), 1 mM PMSF and 1 µM pepstatin A. Lysozyme was added to the homogenates at a concentration of 1.3 mg per gram of cells processed, and the resultant mixture was incubated for 30 minutes on ice to lyse the cells. Inclusion bodies were separated from soluble proteins by centrifugation. These pelleted inclusion bodies were washed and pelleted sequentially in (1) Lysis Buffer; (2) 10 mM Na EDTA pH 8, 30% (w/v) sucrose; and (3) water. The washed inclusion bodies were resuspended in 50 mM Tris pH 8, 10 mM Na EDTA, 150 mM NaCl and 3 M urea, and incubated on ice for 1 hour. The inclusion bodies then were separated from the solubilized proteins by centrifugation. The pelleted inclusion bodies were fully solubilized in 7 M guanidine-HCl, 50 mM Tris pH 8, 0.1% (v/v) beta-mercaptoethanol (BME) overnight at 4°C. The solubilized recombinant antigens were clarified by centrifugation, passed through a 0.2 µm filter and stored at ≤-20°C until purified by chromatography.

Example 7
Purification of Recombinant HIV-1 Group O gp41 Antigen by Chromatography

Solubilized HIV-1 Group O recombinant gp41 antigens obtained from Example 6 were purified by a two-step method, as follows. Guanidine-HCl extracts of insoluble antigens were purified by size exclusion chromatography on a Sephacryl S-300 column equilibrated with 50 mM Tris pH 8, 8 M Urea and 0.1% BME (v/v). SDS-polyacrylamide electrophoresis was used to analyze fractions. Fractions containing the recombinant gp41 antigen were pooled and then concentrated by ultrafiltration. The recombinant antigen concentrate was treated with 4% SDS (w/v) and 5% BME (w/v) at room temperature for 3 hours. SDS treated antigen was further purified by size exclusion chromatography on a Sephacryl S-300 column equilibrated with 25 mM Tris pH 8, 0.15 M NaCl, 0.1% v/v BME, 0.1% SDS (w/v). SDS-polyacrylamide electrophoresis was used to analyze the fractions. Fractions containing purified recombinant antigen were pooled, passed through a 0.2 µm filter and stored at -70° C.

Example 8
Preparation of HIV-1 Group M antigen

Cells containing the plasmid pTB319 were grown and induced as described in Example 5. Cells were lysed and inclusion bodies were processed essentially as described in Example 5 of U.S. Patent No: 5,124,255, incorporated herein by reference. The pellet material was subsequently solubilized in SDS, Phosphate, pH 6.8 and then subjected to chromatography on an S-300 column.

Example 9
Preparation of HIV-2 antigen

pHIV-210/XL1-Blue cells (Example 4, hereinabove) were grown and induced as described in Example 5. Cells were lysed with a buffer containing phosphate, $MgCl_2$, Na EDTA, Triton X-100® pH 7.4 supplemented with Benzonase, Lysozyme, and PMSF. Inclusion bodies were separated from soluble proteins by centrifugation. The pellet was washed sequentially with: distilled H_2O; Triton X-100®, deoxycholate, NaCl, Phosphate pH 7.0; 50 mM Phosphate, pH 7.0; urea, SDS in phosphate, pH 7.0 + BME. Proteins were solubilized in SDS, phosphate, pH 7.0 and BME then subjected to chromatography on an S300 column.

Example 10

One-Step Immunochromatographic Assay for Simultaneous Detection and Differentiation of HIV-1 Group M, HIV-1 Group O and HIV-2

A. Reagent preparation

1. A selenium (Se) colloid suspension was prepared substantially as follows: SeO_2 was dissolved in water to a concentration of 0.0625 gm/ml. Ascorbate then was dissolved in water to a concentration of 0.32 gm/ml and heated in a 70°C water bath for 24 hours. The ascorbate solution then was diluted to 0.0065 gm/ml in water. The SeO_2 solution was quickly added to the diluted ascorbate solution and incubated at 42°C. Incubation was ended after a minimum of 42 hours when the absorbance maximum exceeded 30 at a wavelength between 542 nm and 588 nm. The colloid suspension was cooled to 2-8°C, then stored. Selenium colloid suspension is available from Abbott Laboratories, Abbott Park, Illinois (Code 25001).

2. Selenium colloid/antibody conjugates were prepared as follows. The selenium colloid suspension was concentrated to an absorbance of 25 (OD 500-570) in distilled water. Then, 1M MOPS was added to a final concentration of 10 mM pH 7.2. Goat antibodies specific for human IgG Fc region (or other species of antibody specific for human IgG Fc region) were diluted to a concentration of 0.75 mg/ml with 50 mM Phosphate buffer, and the resultant antibody preparation then was added with mixing to the selenium colloid suspension prepared as described hereinabove, to a final antibody concentration of 75µg/ml. Stirring was continued for 40 minutes. Then, 1% (by weight) bovine serum albumin (BSA) was added to the solution, and the selenium colloid/antibody conjugate solution was stirred for an additional 15 minutes and centrifuged at 5000 x g for 90 minutes. Following this, 90% of the supernatant was removed, and the pellet was resuspended with the remaining supernatant. Immediately prior to coating this selenium-IgG conjugate to a glass fiber pad, it was diluted 1:10 with conjugate diluent (1% [by weight] casein, 0.1% [weight] Triton X-405®, and 50 mM Tris, pH 8.2).

3. Procedural control reagent was prepared as a mixture of HIV-1 (group M), HIV-1 (group O), and HIV-2 positive sera, and is utilized on a separate strip device as a positive control of the assay.

4. Negative control reagent used was normal human utilized on a separate test device as a negative control of the assay.

B. Application pad preparation.

The application pad material comprises resin bonded glass fiber paper (Lydall). Approximately 0.1 ml of the prepared conjugate (described in preceding paragraph 2) is applied to the application pad.

C. Chromatographic Material Preparation.

All reagents are applied to a nitrocellulose membrane by charge and deflect reagent jetting. The nitrocellulose is supported by a MYLAR® membrane that is coated with a pressure sensitive adhesive.

The test sample capture reagents were prepared by (a) diluting the specific antigen prepared as described hereinabove to a concentration of 0.5 mg/ml in jetting diluent (100 mM Tris, pH 7.6 with 1% sucrose (by weight), 0.9% NaCl and 5 µg/ml fluorescein) for HIV-1 group O capture reagent (pGO-9/CKS, SEQ ID NO:50), (b) for HIV-1 group M, subgroup B capture reagent (pTB319, SEQ ID NO:56), and (c) for HIV-2 capture reagent (pHIV-210, SEQ ID NO:55). 0.098 µl of a first capture reagent (reagent HIV-1 group M subgroup B; SEQ ID NO:56) was applied to the strip at the designated capture location and constituted one patient capture site. Likewise, 0.098 µl of a second capture reagent (reagent HIV-1 group O; SEQ ID NO:50) was applied to the strip at the designated capture location and constituted one patient capture site, and 0.098 µl of a third capture reagent (reagent HIV-2; SEQ ID NO:55) was applied to the strip at the designated capture location and constituted one patient capture site.

D. Rapid assay for the presence of antibodies to HIV.

A rapid assay for the presence of antibodies to HIV in test samples serum, whole blood, saliva, and urine samples was performed as follows. In a 1.5 ml Eppendorf tube, 5 µl of serum and 600 µl of sample elution buffer (SEB) (containing 50 mM Tris, 1% BSA (w/v), 0.4% Triton X-405® (v/v), 1.5% Casein (w/v), 3% Bovine IgG (w/v), 4% *E. coli* lysate (v/v), [pH 8.2]) was mixed. Four drops of this mixture was applied to the sample well of the STAR housing. Next, 1 µl of serum or whole blood was added to 100 µl of SEB in a well of a microtiter plate, and the nitrocellulose strip was added in the well. Following this, 1 µl of serum or whole blood was spotted in the test device of the invention's sample well directly and 4 drops of SEB was added. When testing saliva, 50 or 75 µl of saliva was added to 50 µl or 25 µl of SEB, respectively, in a well of a microtiter plate, and the nitrocellulose test strip then was added to the well. When testing urine, 50 µl of urine was added to 50 ul of SEB in a well of a microtiter plate, and the nitrocellulose test strip was added in the well. Alternatively, 100 µl of urine was used in the well of a microtiter plate, and the nitrocellulose test strip was added, without using SEB.

The IgG in the sample was bound by the selenium-goat anti-human IgG colloid in the conjugate pad, and the complexes were chromatographed along the length of the nitrocellulose membrane test strips on which the three recombinant antigens pGO-9 CKS SEQ ID NO:50), pTB319 (HIV-1 group M (subgroup B), SEQ ID NO:56) and pHIV210 (HIV-2, SEQ ID NO:55) previously were applied at a concentration of 1 mg/ml using a biodot machine, which provided positive displacement dispensing using precise drop sizes. The test device then was incubated at room temperature for two minutes, and the results were read visually.

E. Spiked Whole Blood Assay.

In a 1.5 ml Eppendorf tube, the equivalent of 1 µl blood from either confirmed positive HIV-1 group O, HIV-1 group M or HIV-2, or confirmed negative for HIV-1 group O, HIV-1 group M or HIV-2 whole blood test sample was added to 5 µl of a confirmed negative HIV-1 group O, HIV-1 group M or HIV-2 serum along with 100 µl of SEB, and mixed. This mixture was applied to the sample well of the test device of the invention.

The IgG in the sample was bound by the selenium-goat anti-human IgG colloid in the conjugate pad, and the complexes were chromatographed along the length of the nitrocellulose membrane test strips on which the three recombinant antigens pGO-9 CKS SEQ ID NO:50), pTB319 (HIV-1 group M (subgroup B), SEQ ID NO:56) and pHIV210 (HIV-2, SEQ ID NO:55) previously were applied at a concentration of 1 mg/ml using a biodot machine, which provided positive displacement dispensing using precise drop sizes. The test device then was incubated at room temperature for two minutes, and the results were read visually.

F. Results.

If antibody to antigen 1 was present in the test sample, a visible reaction was indicated in the capture zone area of antigen 1 and in the assay completion zone, and not in the zones of antigen 2 or antigen 3. If antibody to antigen 2 was present in the test sample, a visible reaction was indicated in the capture zone area of antigen 2 and in the assay completion zone, and not in the zones of antigen 1 or antigen 3. If antibody to antigen 3 was present in the test sample, a visible reaction was indicated in the capture zone area of antigen 3 and in the assay completion zone, and not in the zones of antigen 1 or antigen 2. Also, a negative control should be non-reactive (show no visible reaction) in the zones of antigen 1, antigen 2 and antigen 3, but should be reactive in the assay completion zone. A positive control (known reactive antibody to antigen 1, 2 and/or 3) should be reactive in the zone of the appropriate antigen to which it specifically binds in an antigen/antibody reaction. A result was considered invalid when a positive reaction occurred in one of the antigen capture zones but not in the assay completion zone, and the test was repeated.

(i) *Assaying for Antibodies in Blood, Urine and Saliva.* The blood, urine, and saliva of three patients (identified by patient numbers 0109, 4068, and 4475) were tested on nitrocellulose solid phase devices of the invention as described herein and following the assay protocol as set forth hereinabove. Each blood and urine test sample of each patient 0109, 4068 and 4475 was reactive with antigen 1 (pTB319; SEQ ID NO:56). The saliva test sample of patients 4068 and 4475 also were reactive with antigen 1, while patient 0109's saliva test sample was non-reactive in the test device of the invention. The saliva test sample of patient 0109 was later retested by a standard EIA and confirmed non-reactive for antibodies to HIV-1 gp41, indicating that the results obtained for the saliva test sample of patient 0109 were valid.

(ii) *Assaying Negative Samples for HIV Antibodies.* Two negative sera and two negative whole blood test samples, each spiked with the same two negative sera, were tested. Samples contained no antibodies specific for the relevant antigens and the test samples were negative after assay on the test (i.e. no reactivity, as indicated by no visible bar signifying a reaction in either position O, M or 2). Test sample was present in each test device, as indicated by a positive reaction bar in the test sample reactivity zone.

(iii) *Assaying for HIV-1 Group M Antibody.* Five HIV-1 Group M sera and five whole blood samples spiked with the HIV-1 Group M positive sera were tested using ten devices. HIV-1 Group M samples were seen to contain antibodies specific for HIV-1 Group M antigen (pTB319) as shown by development of a reaction line at the HIV-1 Group M antigen zone, and visible reaction lines could be seen in the assay completion zone of nine out of 10 test devices. Although a band was present in one particular test device in the capture zone for HIV-1 group M antibody, test sample did not reach the assay completion zone and, thus, the assay needed to be repeated for this particular sample. No cross-reactivity was observed with the capture reagents for HIV group O and HIV-2.

(iv) *Assaying for HIV-1 Group O Antibodies.* Two confirmed positive HIV-1 Group O sera and two whole blood test samples spiked with HIV-1 Group O sera were tested using an additional four devices. The HIV-1 Group O samples were found to contain antibodies specific for HIV-1 Group O antigen as indicated by a positive bar result in the HIV-1 Group O antigen capture zone area, with reaction lines visible in the assay completion zone of each device. No cross-reaction with HIV-1 group M or HIV-2 capture antigens (no visible bar) was observed.

(v) *Assaying for HIV-2 Antibodies.* Ten further test devices were used to test five HIV-2 confirmed positive sera and whole blood spiked with the 5 HIV-2 sera. The HIV-2 samples were found to contain antibodies specific for HIV-2 antigen (pHIV210) as shown by reaction bars at the HIV-2 antigen zone. No reaction was observed between these test samples and the HIV-1 Group O or HIV-1 Group M antigens; visible reaction lines were seen in the assay completion zone of each device.

(vi) *Assaying HIV-1 Group M, HIV-1 Group O, HIV-2 and Negative Samples.* Four final devices were used to test an HIV-1 Group M-positive test sample, an HIV-1 Group O-positive test sample, an HIV-2-positive test sample and a negative control sample. The negative test serum did not react with any antigen in the antigen capture zone; the HIV-1 Group M-positive test sample was reactive only with the HIV-1 Group M antigen; the HIV-1 Group O-positive test sample was reactive only with the HIV-1 Group O antigen; and the HIV-2-positive test sample was reactive only with the HIV-2 antigen. Visible reaction lines were seen in the assay completion zone of each device.

The five HIV-1 group M and the two HIV-1 group O test samples used were confirmed seropositive samples which had been previously tested using a commercially-available enzyme

immunoassay (Abbott #3A77) and had been PCR amplified, sequenced and subtyped based on phylogenetic analysis. The five HIV-2 samples used were seropositive using the same EIA and were confirmed as HIV-2-positive samples using an HIV-2 Western blot test (Sanofi).

Example 11

Construction of Synthetic HIV-1 Group M and HIV-1 Group O Hybrid Genes

A. Modification of pTB319

The plasmid pTB319 (U.S. Patent No. 5,124,255, incorporated herein by reference) encodes a truncated gp41 recombinant protein due to a one base deletion within the synthetic HIV-1 Group M gp41 gene resulting in a frame-shift. In order to facilitate the generation of HIV-1 Group M and Group O hybrid gene constructs, site-specific mutagenesis was used to eliminate the frame-shift within the gp41 coding region in pTB319. This was accomplished by sequentially digesting the plasmid pTB319 with the restriction endonucleases Rsr II and Bst XI. The synthetic oligonucleotides pTB319+A (SEQ ID NO:98) and pTB319+T (SEQ ID NO:99) were annealed and ligated into the Rsr II and Bst XI digested pTB319. The ligation product was used to transform supercompetent XL1-Blue cells and the cells were plated on LB agar plates supplemented with 150 μg/ml ampicillin. Colony PCR was used to identify correctly modified clones using the primer combinations pTB-S4 (SEQ ID NO:100) / pTB-S7 (SEQ ID NO:101) and pTB-S4 (SEQUENCE ID NO:100) / 63168 (SEQ ID NO:121). Overnight cultures were established for candidate clones in LB broth supplemented with 3 mM glucose and 200 μg/ml ampicillin for preparation of miniprep DNA. The entire coding region was sequenced using the oligonucleotide primers: 43461 (SEQ ID NO:2), 43285 (SEQ ID NO:1), CKS-1 (SEQ ID NO:30), CKS-3 (SEQ ID NO:32), pTB-S1 (SEQ ID NO:102), pTB-S2 (SEQ ID NO:103), pTB-S3 (SEQ ID NO:104), pTB-S4 (SEQ ID NO:100), pTB-S5 (SEQ ID NO:105), pTB-S6 (SEQ ID NO:106), pTB-S7 (SEQ ID NO:101), and pTB-S8 (SEQ ID NO:28). Based on sequencing results, clone pTB319+A-#31 (pGMcks-1) has the desired coding region sequence. This clone was subsequently designated as pGM-1CKS/XL1 (SEQ ID NO:107 presents the nucleotide sequence of the coding region). Figure 12 presents the amino acid sequence of the pGM-1CKS recombinant protein (SEQ ID NO:108).

B. Construction of pGO-12CKS/XL1

pGO-12CKS/XL1 encodes the recombinant protein pGO-12CKS, the amino acid sequence of which (SEQ ID NO:91) is shown in Figure 13. This protein consists of 250 amino acids of CKS/polylinker fused to 42 amino acids of *env* gp120 (HIV-1 Group M, HXB2R isolate), 200 amino acids of *env* gp41 (HIV-1 Group M, HXB2R isolate), 45 amino

acids of *env* gp120 (HIV-1 Group O, HAM112 isolate), and 199 amino acids of *env* gp41 (HIV-1 Group O, HAM112 isolate). pGO-12CKS/XL1 was constructed as follows:

A PCR reaction (100 µl volume) was set up with UlTma DNA Polymerase (3U) and 1X buffer along with 1.5mM $MgCl_2$, 40µM of each dNTP, 50pmol of pTB/O-5' (SEQ ID NO:109), 50 pmol pGO-9/Kpn (SEQ ID NO:110), and 1 ng pG0-9PL DNA (miniprep H5; obtained from Example 3, Section F above) as template. The reaction was incubated at 94°C for 105 seconds then amplified with 22 cycles of 94°C for 30 seconds, 55°C for 30 seconds, and 72°C for 75 seconds, followed by incubation at 72°C for 5 minutes. The pTB/O-5' / pGO-9/Kpn PCR product was isolated on gel. The pTB/O-5' / pGO-9/Kpn PCR product and pGM-1CKS plasmid (described in Section A hereinabove) were digested sequentially with Asp 718 (Boehringer Mannheim Biochemicals) and Bst XI. The digested vector was then treated with calf intestinal alkaline phosphatase (Boehringer Mannheim Biochemicals), extracted with phenol / chloroform, and precipitated with ethanol. The digested PCR product was purified on a Centri-Sep column (Princeton Separations). Digested PCR product was ligated into the digested and phosphatased pGM-1CKS vector overnight at 16°C. XL1-Blue supercompetent cells were transformed with the ligation product and plated on LB + ampicillin plates supplemented with 20 mM glucose. Colonies were restreaked for isolation on the same type of plates. An overnight culture (LB medium + 100µg/ml carbenicillin + 20 mM glucose) of clone pGO-12CKS clone #1 was set up. Frozen stocks (0.5 ml 80% glycerol + 0.5 ml overnight culture) were made and miniprep DNA was prepared for sequencing. The following oligonucleotides were used as primers for sequence analysis: CKS-1 (SEQ ID NO:30), CKS-2 (SEQ ID NO:31), CKS-3 (SEQ ID NO:32), CKS-4 (SEQ ID NO:33), CKS 176.1 (SEQ ID NO:19), 3962 (SEQ ID NO:111), 3965 (SEQ ID NO:113), pTB-S2 (SEQ ID NO:103), pTB-S3 (SEQ ID NO:104), pTB-S4 (SEQ ID NO:100), pTB-S5 (SEQ ID NO:105), sy120-S1 (SEQ ID NO:112), 41sy-1B (SEQ ID NO:29), 41sy-2B (SEQ ID NO:34), 41sy-4 (SEQ ID NO:23), pTB-S8 (SEQ ID NO:28). Based on the results of the sequence analysis, pGO-12CKS candidate clone #1 was designated as pGO-12CKS/XL1. (SEQ ID NO:90 presents the nucleotide sequence of the coding region, and SEQ ID NO:91 presents the encoded amino acid sequence.)

C. Construction of pGO-13CKS/XL1

pGO-13CKS/XL1 encodes the recombinant protein pGO-13CKS, the amino acid sequence of which (SEQ ID NO:93) is shown in Figure 14. This protein consists of 250 amino acids of CKS/polylinker fused to 42 amino acids of *env* gp120 (HIV-1 Group M, HXB2R isolate), 200 amino acids of *env* gp41 (HIV-1 Group M, HXB2R isolate), 45 amino

acids of *env* gp120 (HIV-1 Group O, HAM112 isolate), and 169 amino acids of *env* gp41 (HIV-1 Group O, HAM112 isolate). pGO-13CKS/XL1 was constructed as follows:

A PCR reaction (100 µl volume) was set up with UlTma DNA Polymerase (3U) and 1X buffer along with 1.5mM $MgCl_2$, 40µM of each dNTP, 50pmol of pTB/O-5' (SEQ ID NO:109), 50 pmol pGO-8/Kpn (SEQ ID NO:114), and 1 ng pG0-9PL DNA (miniprep H5; obtained from Example 3, Section F hereinabove) as template. The reaction was incubated at 94°C for 105 seconds then amplified with 22 cycles of 94°C for 30 seconds, 55°C for 30 seconds, and 72°C for 75 seconds, followed by incubation at 72°C for 5 minutes. The pTB/O-5' / pGO-8/Kpn PCR product was isolated on gel. The pTB/O-5' / pGO-8/Kpn PCR product and pGM-1CKS plasmid (described in Section A above) were digested sequentially with Asp 718 (Boehringer Mannheim Biochemicals) and Bst XI. The digested vector was then treated with calf intestinal alkaline phosphatase (Boehringer Mannheim Biochemicals), extracted with phenol / chloroform, and precipitated with ethanol. The digested PCR product was purified on a Centri-Sep column (Princeton Separations). Digested PCR product was ligated into the digested and phosphatased pGM-1CKS vector overnight at 16°C. XL1-Blue supercompetent cells were transformed with the ligation product and plated on LB + ampicillin plates supplemented with 20 mM glucose. Colonies were restreaked for isolation on the same type of plates. An overnight culture (LB medium + 100µg/ml carbenicillin + 20 mM glucose) of clone pGO-13CKS clone #1 was set up. Frozen stocks (0.5 ml 80% glycerol + 0.5 ml overnight culture) were made and miniprep DNA was prepared for for sequencing. The following oligonucleotides were used as primers for sequence analysis: CKS-1 (SEQ ID NO:30), CKS-2 (SEQ ID NO:31), CKS-3 (SEQ ID NO:32), CKS-4 (SEQ ID NO:33), 43461 (SEQ ID NO:2), 43285 (SEQ ID NO:1), pTB-S1 (SEQ ID NO:102), pTB-S2 (SEQ ID NO:103), pTB-S3 (SEQ ID NO:104), pTB-S4 (SEQ ID NO:100), pTB-S5 (SEQ ID NO:105), sy120-S1 (SEQ ID NO:112), 41sy-1B (SEQ ID NO:29), 41sy-2B (SEQ ID NO:34), 41sy-4 (SEQ ID NO:23), pTB-S8 (SEQ ID NO:28). Based on the results of the sequence analysis, pGO-13CKS candidate clone #1 was designated as pGO-13CKS/XL1. (SEQ ID NO:92 presents the nucleotide sequence of the coding region, and SEQ ID NO:93 presents the encoded amino acid sequence.)

D. Construction of pGO-14PL/DH5α

pGO-14PL/DH5α encodes the recombinant protein pGO-14PL, the amino acid sequence of which (SEQ ID NO:95) is shown in Figure 15. This protein consists of an N-terminal methionine followed by 45 amino acids of *env* gp120 (HIV-1 Group O, HAM112 isolate), 200 amino acids of *env* gp41 (HIV-1 Group O, HAM112 isolate) fused to 42 amino

acids of *env* gp120 (HIV-1 Group M, HXB2R isolate), and 200 amino acids of *env* gp41 (HIV-1 Group M, HXB2R isolate). pGO-14PL/DH5α was constructed as follows:

A PCR reaction (100 µl volume) was set up with UlTma DNA Polymerase (3U) and 1X buffer along with 1.5mM $MgCl_2$, 40µM of each dNTP, 50pmol of pTB/Age5' (SEQ ID NO:115), 50 pmol pGO/B-3' (SEQ ID NO:116), and 1 ng pGM-1CKS DNA (miniprep of pTB319+A-#31; obtained from Section A above) as template. The reaction was incubated at 95°C for 30 seconds then amplified with 22 cycles of 94°C for 30 seconds, 55°C for 30 seconds, and 72°C for 60 seconds, followed by incubation at 72°C for 5 minutes. The pTB/Age5' / pGO/B-3' PCR product was isolated on gel. The pTB/Age5' / pGO/B-3' PCR product and pGO-9PL plasmid (obtained from Example 3, Section F hereinabove) were digested sequentially with Age I and Bam HI. The digested vector was then treated with calf intestinal alkaline phosphatase (Boehringer Mannheim Biochemicals), extracted with phenol / chloroform, and precipitated with ethanol. The digested PCR product was purified on a Centri-Sep column (Princeton Separations). Digested PCR product was ligated into the digested and phosphatased pGM-1CKS vector overnight at 16°C. DH5α competent cells were transformed with the ligation product and plated on LB + ampicillin (150 µg/ml) plates. Colonies were analyzed for the presence of the proper insert by colony PCR using the vector primers pKRR EcoR1 forward (SEQ ID NO:38) and pKRR BamH1 reverse (SEQ ID NO:39). Colonies containing candidate clones were restreaked for isolation on the same type of plates. Overnight cultures (LB medium + 100µg/ml carbenicillin) were set up to generate frozen stocks and miniprep DNA. Frozen stocks (0.5 ml 80% glycerol + 0.5 ml overnight culture) were made and miniprep DNA was prepared for sequencing. The following oligonucleotides were used as primers for sequence analysis: pTB-S1 (SEQ ID NO:102), pTB-S2 (SEQ ID NO:103), pTB-S3 (SEQ ID NO:104), pTB-S4 (SEQ ID NO:100), pTB-S5 (SEQ ID NO:105), 41sy-1C (SEQ ID NO:40), 41sy-2 (SEQ ID NO:41), 41sy-3 (SEQ ID NO:42), 41sy-4 (SEQ ID NO:23), pKRREcoR1 forward (SEQ ID NO:38), pKRR BamH1 reverse (SEQ ID NO:39). Based on the results of the sequence analysis, pGO-14PL candidate clone #11 was designated as pGO-14PL/DH5α. (SEQ ID NO:94 presents the nucleotide sequence of the coding region, and SEQ ID NO:95 presents the encoded amino acid sequence.)

Example 12

Construction of a HIV-1 Group O *env* gp120 / gp41 Synthetic Gene with a Second Copy of the gp41 Immunodominant Region (IDR) Fused to the C-terminus

A. Construction of pGO-15CKS/XL1

pGO-15CKS/XL1 encodes the recombinant protein pGO-15CKS, the amino acid sequence of which (SEQ ID NO:97) is shown in Figure 16. This protein consists of 246 amino acids of CKS/polylinker fused to 45 amino acids of *env* gp120 (HIV-1 Group O, HAM112 isolate), 199 amino acids of *env* gp41 (HIV-1 Group O, HAM112 isolate), followed by a 4 amino acid linker (Gly, Gly, Gly, Ser) and 32 amino acids encompassing the IDR region of *env* gp41 (HIV-1 Group O, HAM112 isolate). pGO-15CKS/XL1 was constructed as follows:

The plasmid pGO-11CKS propagated in XL1-Blue cells (obtained from Example 3, Section K) was digested sequentially with Age I and Bam HI, extracted with phenol / chloroform, and precipitated with ethanol. The synthetic oligonucleotides synIDR#2-A (SEQ ID NO:117) and synIDR#2-B (SEQ ID NO:118) were kinased with polynucleotide kinase (Boehringer Mannheim Biochemicals) following the manufacturer's recommended procedure. The kinased oligonucleotides were annealed and the duplex ligated to the digested (Age I + Bam HI) pGO-11CKS vector. Supercompetent XL1-Blue cells were transformed with the ligation product, and the cells were plated on LB plates supplemented with 150 µg/ml ampicillin and incubated overnight. Colony PCR (primers 41sy-1B SEQ ID NO:29 and pTB-S8 SEQ ID NO:28) was used to identify candidate clones. Colonies were restreaked for isolation on LB plates supplemented with 150 µg/ml ampicillin. Overnight cultures of the candidate clones were established in 2X LB broth (Life Technologies, Inc.) supplemented with 100 mg/ml carbenicillin and 20 mM glucose (Sigma Chemical Co.). Miniprep DNA was prepared from the overnight cultures using a Promega 373 DNA isolation kit (Promega Corporation, Madison, WI) following the manufacturer's recommended procedure. The overnight cultures were also used to establish frozen stocks. Cells were pelleted and resuspended in 2X LB broth with 20% glycerol (J.T. Baker, Phillipsburg, NJ) and frozen at -70°C. The following oligonucleotide primers were used for sequence analysis: CKS-1 (SEQ ID NO:30), CKS-3 (SEQ ID NO:32), 43285 (SEQ ID NO:1), 43461 (SEQ ID NO:2), 41sy-1B (SEQ ID NO:29), 41sy-2B (SEQ ID NO:34), 41sy-3B (SEQ ID NO:35), 41sy-4 (SEQ ID NO:23), and CKS3583 (SEQ ID NO:20). Based on sequencing results, candidate clone pGO-15CKS-48 was designated as pGO-15CKS/XL1. (SEQ ID NO:96 presents the nucleotide sequence of the coding region, and SEQ ID NO:97 presents the encoded amino acid sequence.)

B. Construction of pGO-15PL/DH5α.

pGO-15PL/DH5α encodes the recombinant protein pGO-15PL, the amino acid sequence of which (SEQ ID NO:120) is shown in Figure 17. This protein consists of an N-terminal methionine followed by 45 amino acids of *env* gp120 (HIV-1 Group O, HAM112 isolate), 199 amino acids of *env* gp41 (HIV-1 Group O, HAM112 isolate), a 4 amino acid linker (Gly, Gly, Gly, Ser) and 32 amino acids encompassing the IDR region of *env* gp41 (HIV-1 Group O, HAM112 isolate). pGO-15PL/DH5 was constructed as follows:

A PCR reaction (100 µl volume) was set up with AmpliTaq DNA Polymerase (2.5U) and 1X buffer along with 40µM of each dNTP, 50pmol of 41sy-3B (SEQ ID NO:35), 50 pmol pTB-S8 (SEQ ID NO:28), and 1 ng pGO-15CKS DNA (miniprep of candidate clone pGO-15CKS-48; obtained from Section A above) as template. The reaction was incubated at 95°C for 30 seconds, then amplified with 35 cycles of 94°C for 20 seconds, 50°C for 30 seconds, and 72°C for 60 seconds, followed by incubation at 72°C for 7 minutes. The amplified product was purified using a QIAquick PCR Purification Kit (Qiagen). The purified 41sy-3B / pTB-S8 amplification product was digested sequentially with Age I and Bam HI, then ligated to pGO-9PL (Age I + Bam HI digested / phosphatased vector prep from Example 3, Section J above). Competent DH5α cells were transformed using the ligation product and plated on LB plates supplemented with 150 µg/ml ampicillin. Candidate clones were identified by colony PCR with the primers 41sy-3 (SEQ ID NO:42) and pKRR BamHI reverse (SEQ ID NO:39), followed by digestion of the PCR product with Age I. Candidate clone #4 was restreaked for isolation. A culture of clone #4 was established in 2X LB broth (Life Technologies) supplemented with 100 µg/ml carbenicillin (Sigma Chemical Co.) and incubated at 34°C overnight. Miniprep DNA was prepared from part of the overnight culture using a Promega 373 DNA Isolation Kit (Promega Corp.) as outlined by the manufacturer. Frozen stocks were established by pelleting the remaining overnight culture and resuspending the cells in Terrific Broth with 20% glycerol (J.T. Baker Co.) and freezing at -70°C. The following oligonucleotide primers were used for sequence analysis: pKRR EcoR1 forward (SEQ ID NO:38), pKRR BamHI reverse (SEQ ID NO:39), 41sy-1C (SEQ ID NO:40), 41sy-2 (SEQ ID NO:41), 41sy-3 (SEQ ID NO:42), 41sy-3B (SEQ ID NO:35) and 41sy-4 (SEQ ID NO:23). Based on sequencing results, candidate pGO-15PL clone #4 was designated as pGO-15PL/DH5α. (SEQ ID NO:119 presents the nucleotide sequence of the coding region, and SEQ ID NO:120 presents the encoded amino acid sequence.)

Example 13

Preparation and Purification of HIV-1 Group O Recombinant gp41 Antigens pGO-8 PL, pGO-9 PL, pGO-12CKS, pGO-14 PL and pGO-15CKS

The above antigens were prepared by growing and inducing *E. coli* strains containing the respective HIV-1 Group O recombinant gp41 antigen constructs as described in Example 5. The resulting frozen cells were resuspended by homogenization in cold lysis buffer comprising 50 mM Tris pH 8, 10 mM Na EDTA , 150 mM NaCl , 8% (w/v) sucrose, 5% Triton X-100 ® (v/v), 1 mM PMSF and 1 µM pepstatin A. Lysozyme was added to the homogenates at a concentration of 1.3 mg per gram of cells processed, and incubated for 30 minutes on ice to lyse the cells. Inclusion bodies were separated from soluble proteins by centrifugation. These pelleted inclusion bodies were washed and pelleted sequentially in 1) Lysis Buffer; 2) 10 mM Na EDTA pH 8, 30% (w/v) sucrose; and 3) water. The washed inclusion bodies were resuspended in 50 mM Tris pH 8, 10 mM Na EDTA, 150 mM NaCl and 3 M urea, and incubated on ice for 1 hour. The inclusion bodies then were separated from the solubilized proteins by centrifugation. The pelleted inclusion bodies were fully solubilized in 7 M guanidine-HCl, 50 mM Tris pH 8, 0.1% (v/v) beta-mercaptoethanol (BME) overnight at 4°C. The solubilized recombinant antigen(s) were clarified by centrifugation, passed through a 0.2 µm filter. The solubilized gp41 antigen(s) were precipitated from the 7 M Guanidine-HCl solution by dilution (1:7) with water to a final concentration of 1 M Guanidine-HCl. After incubation at 4° C for 30 minutes, the precipitated proteins were centrifuged and resolubilized in 50 mM Tris pH 8, 9 M Urea, 0.1% BME (v/v) overnight at 4° C.

Solubilized HIV-1 Group O recombinant gp41 antigens were next purified as follows: The recombinant antigens were first purified by anion and/or cation exchange chromatography using Q-Sepharose (Pharmacia) or S-Sepharose (Pharmacia) columns. The solubilized gp41 antigen solutions were loaded onto either a Q-Sepharose or S-Sepharose column that had been previously equilibrated with 50 mM Tris pH 8, 8M Urea, 0.1% BME (v/v). The gp41 antigens either (1) passed though the column directly and were collected in the void volume or (2) were bound to the column matrix. If adsorbed, the gp41 antigens were eluted from the columns by a 0-1M NaCl gradient. SDS-polyacrylamide gel electrophoresis was used to analyze fractions from the Q-Sepharose or S-Sepharose columns. Fractions containing the recombinant gp41 antigens were pooled and then concentrated by ultrafiltration. The recombinant antigen concentrates were treated with 4% SDS (w/v) and 5% BME (w/v) at room temperature for three hours. SDS treated antigens were further purified by size exclusion chromatography on a Sephacryl S-300 (Pharmacia) column equilibrated with 25 mM Tris pH 8, 0.15 M NaCl, 0.1% v/v BME, 0.1% SDS (w/v). SDS-polyacrylamide gel electrophoresis was used to analyze the fractions from the S-300 column. Fractions containing purified recombinant antigens were pooled, passed through a 0.2 µm filter and stored at -70° C.

Example 14

Test of Recombinant Antigen Reactivity with HIV-1 Group M and Group O Samples

A. Bead Coating

In order to examine the reactivity of recombinant HIV-1 antigens, purified recombinants were coated on quarter inch polystyrene beads. These antigen coated beads were used in a series of capture assays to access reactivity to both HIV-1 Group M and Group O samples.

Recombinant antigens were coated on quarter inch beads at 0.5 µg/ml in PBS. The following recombinant antigens were coated: pTB319 (Group M), pGO-9/CKS, pGO-11/PL, pGO-12/CKS, pGO-14/PL and pGO-15/CKS (all Group O).

The procedure for coating the recombinant antigens on the beads is as follows: For each antigen, 35.5 gm. (~250) of beads, (Abbott Laboratories code 93-2556, lot 6840M100), were washed in 15% N-propanol in water for 30 minutes at 40°C. All incubations and washes were done in small brown glass jars on a shaker platform. The N-propanol solution was aspirated off, 58.25 ml of antigen solution was added, and the beads were incubated for two hours at 40°C. The antigen solution was aspirated off, and 60 ml of a 0.1% Triton X-100 solution in PBS was added for 30 minutes at 40°C. The beads were then washed with 60 ml of PBS two times and incubated with 60 ml of 2% BSA in PBS for 30 minutes at 40°C. The BSA was aspirated and the beads were washed again in PBS. The beads were then incubated with 60 ml 0.5% sucrose in PBS for 15 minutes at room temperature. After 15 minutes, the sucrose was aspirated and the beads were allowed to air dry. Coated beads were strored in polypropylene bottles with a desiccant at 4°C.

B. Assays

Recombinant antigen coated beads were tested for reactivity against a variety of samples using the Abbott Laboratories 3A11 kit (first generation, indirect assay format). Samples were diluted and added to wells in polystyrene trays. Beads were added and the trays were incubated at 40°C for 1 hour. The trays were washed with water in an Abbott Laboratories QUICKWASH device. Next the kit conjugate, an anti-human IgG-Horseraddish Peroxidase, was added and the trays were again incubated at 40°C for one hour. The trays were again washed and 300 µl of substrate solution, (1.28 mg/ml o-Phenylenediamine•HCl in Citrate-Phosphate buffer containing 0.02% Hydrogen Peroxide), was added to each well for 30 minutes at room temperature. 1 ml of 1N sulfuric acid was added to stop the reaction, and the trays were read in an Abbott QUANTUM spectrophotometer.

The samples used for this study were Normal human plasma, (Abbott Laboratories code 99800, lot 17535M400), used as a negative control; HIVPL-31 (Group M positive sera),

and the following Group O positive sera: 14283, 189404, 193Ha, 14791, 267Ha and ESP-1. All samples except the Normal human plasma control were run at three dilutions; 1:1,000, 1:10,000 and 1:100,000 in the kit specimen diluent. Each dilution of each sample was run in duplicate against each of the six beads, and the results of each dilution were averaged and plotted for each bead.

C. Results

The results of the above tests, shown in Figures 18-23, demonstrate the improvements in sensitivity and selectivity available by use of the recombinant antigens of the present invention. The bead coated with the HIV-1 Group M recombinant antigen (pTB319) detected the Group M serum sample, but failed to detect all but one of the Group O samples. The beads coated with only HIV-1 Group O recombinant antigens (pGO-9/CKS, pGO-11/PL, and PGO-15/CKS) detected the Group O serum samples, but showed lower sensitivity in detection of the HIV-1 Group M sample. Beads that were coated with hybrid Group M and Group O recombinant antigens (pGO-12/CKS, and pGO-14/PL) were able to detect both HIV-1 Group M- and Group O-positive samples. Lastly, pGO-15/CKS, which has an additional sequence representing the Group O immunodominant region of gp41 linked by recombinant means to the carboxy end of the protein, showed greater reactivity to low-titer Group O samples.

Example 15

Examination of Assay Sensitivity for HIV-1 Group O-Infected Samples Using Group O Recombinant Antigens pGO-9CKS and pGO-11CKS

A. Assays

In order to evaluate the performance in immunoassays of antigen constructs of the present invention, recombinant antigens pGO-9CKS and pGO-11CKS were incorporated into four HIV-1/HIV-2 immunoassays containing HIV-1 Group M (subtype B) reagents. The constructs were tested using one bead assay (Assay 1) and 3 automated microparticle-based assays (Assays 2-4). In all cases, the reactivity of HIV-1 Group O-infected specimens was assessed with (format 2) and without (format 1) incorporation of the HIV-1 group O recombinants. The coated beads/microparticles were reacted with multiple dilutions of the following HIV-1 Group O-positive human sera: ESP1, 189404, 193Ha, 341 Ha, 2156 and ABB 9/96.

For Assay 1, purified pGO-11CKS was incorporated into a commercially-available bead-based assay by coating the antigen construct onto quarter-inch polystyrene beads. The coated beads were reacted with a range of dilutions of HIV-1 Group O-positive human sera, washed, and then reacted with purified pGO-9CKS conjugated to horseradish peroxidase.

After washing/separation of bound from unbound pGO-9CKS conjugate, substrate was added and the assay was completed as indicated in Example 14.

For Assay 2, purified pGO-11CKS was incorporated into a second commercially-available assay by coating the antigen construct onto microparticles. The coated microparticles were reacted with the same range of dilutions of HIV-1 Group O-positive human sera utilized in Assay 1. The microparticles were then washed and subsequently reacted with biotinylated pGO-9CKS. After further washing, the microparticles were reacted with a polyclonal anti-biotin antibody conjugated to alkaline phosphatase. The assay signal was developed by addition of the substrate methylumbelliferyl phosphate.

For Assay 3, purified pGO-11CKS was incorporated into a third commercially-available assay by coating the antigen construct on microparticles. The coated microparticles were again reacted with the same range of dilutions of HIV-1 Group O-positive human sera utilized in Assay 1. Next, the microparticles were washed and then reacted with biotinylated pGO-9CKS. After washing, the microparticles were reacted with an anti-biotin antibody conjugated to acridinium as the signal-generating compound.

For Assay 4, purified pGO-11CKS was incorporated into a developmental assay by coating the antigen construct onto magnetic microparticles. As in Assay 1, the coated microparticles were reacted with a range of dilutions of HIV-1 Group O-positive human sera, washed, and subsequently reacted with pGO-9CKS conjugated to acridinium.

B. Results

The results of the above tests are presented in Tables 1 and 2 below, in which the data are presented as signal/cutoff (S/CO) ratios. Format 1 refers to the conventional assay without the antigen constructs of the present invention, while Format 2 refers to the assay supplemented with the HIV-1 group O constructs.

From these data, it can be seen that the addition of the HIV-1 Group O recombinants resulted in a significant enhancement of assay sensitivity for the HIV-1 Group O-infected sera at all of the dilutions tested. For example, in the case of Assay 1 and sample 193Ha a S/CO ratio of 7.14 was obtained at a 1:10 dilution using Format 1, while a similar S/CO (7.22) was obtained at a 160-fold greater dilution (1:1600) using Format 2. This trend was maintained across all of the tested assay platforms. The utility of the group O recombinants was particularily evident for sample 2156, which tested negative (S/CO < 1) in all 4 assays prior to the addition of the group O recombinants. With the addition of the HIV-1 Group O constructs, however, this sample 2156 tested positive in all four assays at a 1:400 dilution. In Assay 1, 2156 was still positive at a dilution of 1:5000. Addition of the recombinant reagents pGO-9CKS and pGO-11CKS was thus seen to provide a substantially better sensitivity for HIV-1 Group O-infected sera when using the above direct-format immunoassays.

Table 1

		Assay 1		Assay 2		Assay 3		Assay 4	
		Format 1	Format 2	Format 1	Format 2	Format 1	Format 2	Format 1	Format 2
193Ha	1:10	7.14	16.92	3.67	10.05	9.65	37.57	0.93	8.99
	1:100	1.85	16.92	0.87	6.08	1.70	25.89	0.61	4.81
	1:200	1.00	16.92	0.66	5.03	1.18	23.57	0.54	4.07
	1:400	0.86	16.92	0.53	4.03	0.78	18.40	0.54	2.62
	1:800	0.39	12.41	0.41	2.56	0.59	13.00	0.55	1.74
	1:1600	0.24	7.22	0.39	1.74	0.53	8.02	0.56	1.16
	1:5000	0.09	2.14	NT	NT	0.37	3.33	NT	NT
	1:10000	0.05	1.55	NT	NT	0.38	1.69	NT	NT
341HA	1:10	7.41	16.92	15.36	13.52	50.27	82.28	3.06	10.43
	1:100	3.34	16.92	7.30	9.78	13.25	55.32	1.34	7.09
	1:200	2.04	16.92	4.75	8.43	8.00	42.66	1.01	6.78
	1:400	1.32	16.92	2.57	6.66	4.41	31.89	0.90	4.83
	1:800	0.93	16.92	1.49	5.25	2.45	25.47	0.70	3.17
	1:1600	0.50	11.41	0.92	3.84	1.26	17.48	0.63	2.50
	1:5000	0.25	5.01	NT	NT	0.74	8.16	NT	NT
	1:10000	0.12	1.68	NT	NT	0.48	4.56	NT	NT
2156	1:10	0.25	16.92	0.49	5.33	0.37	20.79	0.63	5.52
	1:100	0.11	14.89	0.44	3.46	0.42	14.00	0.54	2.41
	1:200	0.01	10.07	0.36	2.45	0.39	9.92	0.62	1.59
	1:400	0.13	5.93	0.38	1.65	0.38	6.01	0.53	1.13
	1:800	0.04	3.45	0.36	1.12	0.41	3.65	0.51	0.85
	1:1600	0.01	1.91	0.40	0.75	0.44	2.12	0.54	0.66
	1:5000	0.08	1.11	NT	NT	0.39	0.97	NT	NT
	1:10000	0.15	0.45	NT	NT	0.37	0.70	NT	NT

Table 2

	Assay 1		Assay 2		Assay 3		Assay 4	
	Format 1	Format 2	Format 1	Format 2	Format 1	Format 2	Format 1	Format 2
ABB 9/96 1:10	3.17	16.92	4.39	9.64	8.96	35.65	1.55	7.76
1:100	1.67	16.90	0.83	6.00	2.33	28.06	0.75	4.43
1:200	1.35	16.90	0.66	5.43	1.57	25.03	0.60	4.01
1:400	1.12	16.90	0.52	4.19	1.13	21.90	0.59	3.20
1:800	0.88	13.25	0.49	3.59	0.85	17.86	0.58	2.15
1:1600	0.48	9.19	0.40	2.63	0.65	12.87	0.55	1.50
1:5000	0.40	4.95	NT	NT	0.53	6.52	NT	NT
1:10000	0.17	1.39	NT	NT	0.43	3.58	NT	NT
ESP1 1:10	9.18	16.92	9.69	12.30	15.78	44.37	2.87	12.46
1:100	1.06	16.92	2.78	6.88	2.08	22.02	0.77	5.12
1:200	0.52	16.92	1.41	5.32	1.19	17.66	0.65	3.38
1:400	0.26	16.92	0.87	3.90	0.79	13.38	0.60	2.59
1:800	0.09	12.59	0.67	2.67	0.53	9.45	0.52	1.62
1:1600	0.20	8.35	0.52	1.76	0.46	5.66	0.56	1.06
1:5000	0.08	3.31	NT	NT	0.57	2.36	NT	NT
1:10000	0.09	2.05	NT	NT	0.37	1.34	NT	NT
189404 1:10	20.76	16.92	20.44	14.98	31.64	37.47	3.58	9.78
1:100	10.37	16.92	8.12	7.83	12.19	24.67	1.26	4.60
1:200	8.10	15.72	5.37	5.71	8.36	19.86	1.12	3.51
1:400	4.38	11.61	3.11	4.10	5.33	14.20	0.76	2.32
1:800	2.28	7.81	1.78	2.80	2.94	10.42	0.73	1.75
1:1600	1.34	4.55	1.03	1.66	1.81	6.12	0.57	1.21
1:5000	0.40	1.96	NT	NT	0.94	2.49	NT	NT
1:10000	0.26	1.00	NT	NT	0.59	1.58	NT	NT

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hackett, John R. Jr.
Yamaguchi, Julie
Golden, Alan M.
Brennan, Catherine A.
Hickman, Robert K.
Devare, Sushil G.

(ii) TITLE OF THE INVENTION: Recombinant Antigens Useful In The Detection And Differentiation Of Antibodies To HIV

(iii) NUMBER OF SEQUENCES: 121

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Abbott Laboratories
(B) STREET: 100 Abbott Park Road
(C) CITY: Abbott Park
(D) STATE: IL
(E) COUNTRY: USA
(F) ZIP: 60064-3500

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5 inch Diskette, 1.4MB, DOS-formatted
(B) COMPUTER: Power Macintosh 7100/66
(C) OPERATING SYSTEM: MacOS 7.1.2 (DOS emulation)
(D) SOFTWARE: WordPerfect 3.1 (saved as Text Export, ASCII format)

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Danckers, Andreas M.
(B) REGISTRATION NUMBER: 32,652
(C) REFERENCE/DOCKET NUMBER: 6165.US.01

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 847-937-9803
(B) TELEFAX: 847-938-2623

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAGATCTTCA GGGGTATCC 19

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGATCATCGG TTCATCACCC 20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATGATCGGT GGTGACATGA AAGACATCTG GCGTAACGAA CTGTTCAAAT ACAAAGTTGT 60
TCGTGTTAAA CCGTTCTCTG TTGCTCCGAC CCCGATCGCT CGTCCGGTTA TCGG 114

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCAGGTTCCA CTATGGGTGC TGCAGCTACC GCTCTGACCG TACAGACCCA CTCTGTTATC 60
AAAGGTATCG TACAGCAGCA CGACAACCTG CTGCGTGCAA TCCAGGCACA G 111

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGCTGCTGGT TCTGGATCAG GGTTTCCAGT GCCAGCAGAC GAGCACGCAG CTGACGGATA 60
CCCCATACAG ACAGACGCAG CAGTTCCTGC TGTGCCTGGA TTGCACGCAG 110

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTGATCCAGA ACCAGCAGCT GCTGAACCTG TGGGGCTGCA AAGGTCGTCT GATCTGCTAC 60
ACCTCCGTTA AATGGAACGA AACCTGGCGT AACACCACCA ACATCAACCA G 111

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTGAACCTGA GCTTTCTGGA TTTCTTCGTA GATGGTGGAA GAAACGTTGT CGATCTGCTG 60
GTCCCATTCC TGCCAGGTCA GGTTACCCCA GATCTGGTTG ATGTTGGTGG TGTTACG 117

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TCCAGAAAGC TCAGGTTCAG CAGGAACAGA ACGAAAAAAA ACTGCTGGAA CTGGACGAAT 60
GGGCTTCTCT GTGGAACTGG CTGGACATCA CCAAATGGCT G 101

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACCTTCACCG GTACGACCCG GAGTTTCAGC TTCAGACTGC TGACGGGTCG GGATCTGCAG 60
GGACAGCGGC TGGTAGCCCT GACGGATGTT ACGCAGCCAT TTGGTGATGT CCAG 114

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGGGTCGTAC CGGTGAAGGT GGTGGTGACG AAGGCCGTCC GCGTCTGATC CCGTCTCCGC 60
AGGGTTTCCT GCCGCTGCTG TACACCGACC TGCGTACCAT CATCCTG 107

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTACAAGAAT TCCATGATCG GTGGTGACAT G 31

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTCTGTGGAT TCTGGGTCAG AAAATCATCG ACGCTTGCCG TATCTGCGCT GCTGTTATCC 60
ACTACTGGCT GCAGGAACTG CAGAAATCCG CTACCTCCCT GATCGACAC 109

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCGAACACGA CGCGGGATGT TCAGGATACC ACGACCCAGA CGCTGGATAC CACGGATGAT 60
GTCGTCAGTC CAGTTAGCAA CTGCAACAGC GAAGGTGTCG ATCAGGGAGG TAGC 114

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATAGTAGGAT CCTATTACAG CAGAGAGCGT TCGAAGCCCT GGCGAACACG ACGCGGGATG 60

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATAGTAGGAT CCTATTATTC ACCGGTACGA CCCGGAGTTT CAG 43

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATAGTAGGAT CCTATTACAG CCATTTGGTG ATGTCCAG 38

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCACCCATAG TGGAACCTGC TGCAGACAGA ACGCCCAGGA ACAGCATACC CAGACCTACA 60
GCACGTTTTT CACGGTGGGT GCCAGTACCG ATAACCGGAC GAGCGA 106

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTGACCCAGA ATCCACAGAC CCAGACGCAG GTGAGAGATA ACAGTCTGAG TACCAGAGAT 60
CAGGTTAGAC AGCAGGTGGT AGGACCACAG GATGATGGTA CGCAGGTC 108

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCAGCTTCGT GTTCTGTGGT ACGGCG 26

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGTAACGGTA CGACACTCC 19

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCGCTACCTC CCTGATCGAC ACCTTC 26

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GAAGGTGTCG ATCAGGGAGG TAGCGG 26

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATGTCCAGC CAGTTCCAC 19

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTACAAGAAT TCCATGATCG GTGGTGACAT GAAAGACATC TGGCGTAACG AACTGTTCAA 60
ATAC 64

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTACAAGAAT TCTATCGGTG GTGACATGAA AGAC 34

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CGGGTCGTAC CGGTGAAGGT 20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATAGTAGGAT CCTATTACAG CAG 23

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCCGGAAGCG AGAAGAATC 19

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TATCGTACAG CAGCAGGAC 19

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCCATTAATG TGAGTTAGCT C 21

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCTGACGAAT GATTGTCGCA 20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATTCAGCGAC GACACGGTG 19

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTATCCACAC CTGTGCCA 18

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AGAGTGGGTC TGTACGGTC 19

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AATGGGCTTC TCTGTGGAAC 20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CTGTCTAACC TGATCTCTGG 20

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ACGCAGGTGA GAGATAACAG 20

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GTGATACGAA ACGAAGCATT GG 22

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GCGATATAGG CGCCAGCAAC C 21

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTCTGTTATC AAAGGTATCG T 21

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AGCAGACGAG CACGCAGC 18

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TTCAGCAGGA ACAGAACG 18

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TCCGCGTCTG ATCCCGTC 18

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CCAGGCACAG CAGGAAC 17

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACACTATAGA ATACTCAAGC 20

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAATACGACT CACTATAGGG 20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 741 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATGATCGGTG GTGACATGAA AGACATCTGG CGTAACGAAC TGTTCAAATA CAAAGTTGTT 60
CGTGTTAAAC CGTTCTCTGT TGCTCCGACC CCGATCGCTC GTCCGGTTAT CGGTACTGGC 120
ACCCACCGTG AAAAACGTGC TGTAGGTCTG GGTATGCTGT TCCTGGGCGT TCTGTCTGCA 180
GCAGGTTCCA CTATGGGTGC TGCAGCTACC GCTCTGACCG TACAGACCCA CTCTGTTATC 240
AAAGGTATCG TACAGCAGCA GGACAACCTG CTGCGTGCAA TCCAGGCACA GCAGGAACTG 300
CTGCGTCTGT CTGTATGGGG TATCCGTCAG CTGCGTGCTC GTCTGCTGGC ACTGGAAACC 360
CTGATCCAGA ACCAGCAGCT GCTGAACCTG TGGGGCTGCA AAGGTCGTCT GATCTGCTAC 420
ACCTCCGTTA AATGGAACGA AACCTGGCGT AACACCACCA ACATCAACCA GATCTGGGGT 480
AACCTGACCT GGCAGGAATG GGACCAGCAG ATCGACAACG TTTCTTCCAC CATCTACGAA 540
GAAATCCAGA AAGCTCAGGT TCAGCAGGAA CAGAACGAAA AAAAACTGCT GGAACTGGAC 600
GAATGGGCTT CTCTGTGGAA CTGGCTGGAC ATCACCAAAT GGCTGCGTAA CATCCGTCAG 660
GGCTACCAGC CGCTGTCCCT GCAGATCCCG ACCCGTCAGC AGTCTGAAGC TGAAACTCCG 720
GGTCGTACCG GTGAATAATA G 741

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```
Met Ile Gly Gly Asp Met Lys Asp Ile Trp Arg Asn Glu Leu Phe Lys
 1               5                  10                  15
Tyr Lys Val Val Arg Val Lys Pro Phe Ser Val Ala Pro Thr Pro Ile
            20                  25                  30
Ala Arg Pro Val Ile Gly Thr Gly Thr His Arg Glu Lys Arg Ala Val
        35                  40                  45
Gly Leu Gly Met Leu Phe Leu Gly Val Leu Ser Ala Ala Gly Ser Thr
    50                  55                  60
Met Gly Ala Ala Ala Thr Ala Leu Thr Val Gln Thr His Ser Val Ile
65                  70                  75                  80
Lys Gly Ile Val Gln Gln Gln Asp Asn Leu Leu Arg Ala Ile Gln Ala
                85                  90                  95
Gln Gln Glu Leu Leu Arg Leu Ser Val Trp Gly Ile Arg Gln Leu Arg
            100                 105                 110
Ala Arg Leu Leu Ala Leu Glu Thr Leu Ile Gln Asn Gln Gln Leu Leu
        115                 120                 125
Asn Leu Trp Gly Cys Lys Gly Arg Leu Ile Cys Tyr Thr Ser Val Lys
    130                 135                 140
Trp Asn Glu Thr Trp Arg Asn Thr Thr Asn Ile Asn Gln Ile Trp Gly
145                 150                 155                 160
Asn Leu Thr Trp Gln Glu Trp Asp Gln Gln Ile Asp Asn Val Ser Ser
                165                 170                 175
Thr Ile Tyr Glu Glu Ile Gln Lys Ala Gln Val Gln Gln Glu Gln Asn
            180                 185                 190
Glu Lys Lys Leu Leu Glu Leu Asp Glu Trp Ala Ser Leu Trp Asn Trp
        195                 200                 205
Leu Asp Ile Thr Lys Trp Leu Arg Asn Ile Arg Gln Gly Tyr Gln Pro
    210                 215                 220
Leu Ser Leu Gln Ile Pro Thr Arg Gln Gln Ser Glu Ala Glu Thr Pro
225                 230                 235                 240
Gly Arg Thr Gly Glu
                245
```

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1476 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```
ATGAGTTTTG TGGTCATTAT TCCCGCGCGC TACGCGTCGA CGCGTCTGCC CGGTAAACCA     60
TTGGTTGATA TTAACGGCAA ACCCATGATT GTTCATGTTC TTGAACGCGC GCGTGAATCA    120
GGTGCCGAGC GCATCATCGT GGCAACCGAT CATGAGGATG TTGCCCGCGC CGTTGAAGCC    180
GCTGGCGGTG AAGTATGTAT GACGCGCGCC GATCATCAGT CAGGAACAGA ACGTCTGGCG    240
GAAGTTGTCG AAAAATGCGC ATTCAGCGAC GACACGGTGA TCGTTAATGT GCAGGGTGAT    300
```

```
GAACCGATGA TCCCTGCGAC AATCATTCGT CAGGTTGCTG ATAACCTCGC TCAGCGTCAG    360
GTGGGTATGA CGACTCTGGC GGTGCCAATC CACAATGCGG AAGAAGCGTT TAACCCGAAT    420
GCGGTGAAAG TGGTTCTCGA CGCTGAAGGG TATGCACTGT ACTTCTCTCG CGCCACCATT    480
CCTTGGGATC GTGATCGTTT TGCAGAAGGC CTTGAAACCG TTGGCGATAA CTTCCTGCGT    540
CATCTTGGTA TTTATGGCTA CCGTGCAGGC TTTATCCGTC GTTACGTCAA CTGGCAGCCA    600
AGTCCGTTAG AACACATCGA AATGTTAGAG CAGCTTCGTG TTCTGTGGTA CGGCGAAAAA    660
ATCCATGTTG CTGTTGCTCA GGAAGTTCCT GGCACAGGTG TGGATACCCC TGAAGATCTC    720
GACCCGTCGA CGAATTCTAT CGGTGGTGAC ATGAAAGACA TCTGGCGTAA CGAACTGTTC    780
AAATACAAAG TTGTTCGTGT TAAACCGTTC TCTGTTGCTC CGACCCCGAT CGCTCGTCCG    840
GTTATCGGTA CTGGCACCCA CCGTGAAAAA CGTGCTGTAG GTCTGGGTAT GCTGTTCCTG    900
GGCGTTCTGT CTGCAGCAGG TTCCACTATG GGTGCTGCAG CTACCGCTCT GACCGTACAG    960
ACCCACTCTG TTATCAAAGG TATCGTACAG CAGCAGGACA ACCTGCTGCG TGCAATCCAG   1020
GCACAGCAGG AACTGCTGCG TCTGTCTGTA TGGGGTATCC GTCAGCTGCG TGCTCGTCTG   1080
CTGGCACTGG AAACCCTGAT CCAGAACCAG CAGCTGCTGA ACCTGTGGGG CTGCAAAGGT   1140
CGTCTGATCT GCTACACCTC CGTTAAATGG AACGAAACCT GGCGTAACAC CACCAACATC   1200
AACCAGATCT GGGGTAACCT GACCTGGCAG GAATGGGACC AGCAGATCGA CAACGTTTCT   1260
TCCACCATCT ACGAAGAAAT CCAGAAAGCT CAGGTTCAGC AGGAACAGAA CGAAAAAAAA   1320
CTGCTGGAAC TGGACGAATG GGCTTCTCTG TGGAACTGGC TGGACATCAC CAAATGGCTG   1380
CGTAACATCC GTCAGGGCTA CCAGCCGCTG TCCCTGCAGA TCCCGACCCG TCAGCAGTCT   1440
GAAGCTGAAA CTCCGGGTCG TACCGGTGAA TAATAG                             1476
```

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 490 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```
Met Ser Phe Val Val Ile Ile Pro Ala Arg Tyr Ala Ser Thr Arg Leu
 1               5                  10                  15
Pro Gly Lys Pro Leu Val Asp Ile Asn Gly Lys Pro Met Ile Val His
            20                  25                  30
Val Leu Glu Arg Ala Arg Glu Ser Gly Ala Glu Arg Ile Ile Val Ala
        35                  40                  45
Thr Asp His Glu Asp Val Ala Arg Ala Val Glu Ala Ala Gly Gly Glu
    50                  55                  60
Val Cys Met Thr Arg Ala Asp His Gln Ser Gly Thr Glu Arg Leu Ala
65                  70                  75                  80
Glu Val Val Glu Lys Cys Ala Phe Ser Asp Asp Thr Val Ile Val Asn
                85                  90                  95
Val Gln Gly Asp Glu Pro Met Ile Pro Ala Thr Ile Ile Arg Gln Val
            100                 105                 110
Ala Asp Asn Leu Ala Gln Arg Gln Val Gly Met Thr Thr Leu Ala Val
        115                 120                 125
Pro Ile His Asn Ala Glu Glu Ala Phe Asn Pro Asn Ala Val Lys Val
    130                 135                 140
Val Leu Asp Ala Glu Gly Tyr Ala Leu Tyr Phe Ser Arg Ala Thr Ile
145                 150                 155                 160
Pro Trp Asp Arg Asp Arg Phe Ala Glu Gly Leu Glu Thr Val Gly Asp
                165                 170                 175
Asn Phe Leu Arg His Leu Gly Ile Tyr Gly Tyr Arg Ala Gly Phe Ile
            180                 185                 190
Arg Arg Tyr Val Asn Trp Gln Pro Ser Pro Leu Glu His Ile Glu Met
        195                 200                 205
Leu Glu Gln Leu Arg Val Leu Trp Tyr Gly Glu Lys Ile His Val Ala
    210                 215                 220
```

```
Val Ala Gln Glu Val Pro Gly Thr Gly Val Asp Thr Pro Glu Asp Leu
225                 230                 235                 240
Asp Pro Ser Thr Asn Ser Ile Gly Gly Asp Met Lys Asp Ile Trp Arg
                245                 250                 255
Asn Glu Leu Phe Lys Tyr Lys Val Val Arg Val Lys Pro Phe Ser Val
            260                 265                 270
Ala Pro Thr Pro Ile Ala Arg Pro Val Ile Gly Thr Gly Thr His Arg
        275                 280                 285
Glu Lys Arg Ala Val Gly Leu Gly Met Leu Phe Leu Gly Val Leu Ser
    290                 295                 300
Ala Ala Gly Ser Thr Met Gly Ala Ala Ala Thr Ala Leu Thr Val Gln
305                 310                 315                 320
Thr His Ser Val Ile Lys Gly Ile Val Gln Gln Gln Asp Asn Leu Leu
                325                 330                 335
Arg Ala Ile Gln Ala Gln Gln Glu Leu Leu Arg Leu Ser Val Trp Gly
            340                 345                 350
Ile Arg Gln Leu Arg Ala Arg Leu Leu Ala Leu Glu Thr Leu Ile Gln
        355                 360                 365
Asn Gln Gln Leu Leu Asn Leu Trp Gly Cys Lys Gly Arg Leu Ile Cys
    370                 375                 380
Tyr Thr Ser Val Lys Trp Asn Glu Thr Trp Arg Asn Thr Thr Asn Ile
385                 390                 395                 400
Asn Gln Ile Trp Gly Asn Leu Thr Trp Gln Glu Trp Asp Gln Gln Ile
                405                 410                 415
Asp Asn Val Ser Ser Thr Ile Tyr Glu Glu Ile Gln Lys Ala Gln Val
            420                 425                 430
Gln Gln Glu Gln Asn Glu Lys Lys Leu Leu Glu Leu Asp Glu Trp Ala
        435                 440                 445
Ser Leu Trp Asn Trp Leu Asp Ile Thr Lys Trp Leu Arg Asn Ile Arg
    450                 455                 460
Gln Gly Tyr Gln Pro Leu Ser Leu Gln Ile Pro Thr Arg Gln Gln Ser
465                 470                 475                 480
Glu Ala Glu Thr Pro Gly Arg Thr Gly Glu
                485                 490
```

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```
ATGATCGGTG GTGACATGAA AGACATCTGG CGTAACGAAC TGTTCAAATA CAAAGTTGTT     60
CGTGTTAAAC CGTTCTCTGT TGCTCCGACC CCGATCGCTC GTCCGGTTAT CGGTACTGGC    120
ACCCACCGTG AAAAACGTGC TGTAGGTCTG GGTATGCTGT TCCTGGGCGT TCTGTCTGCA    180
GCAGGTTCCA CTATGGGTGC TGCAGCTACC GCTCTGACCG TACAGACCCA CTCTGTTATC    240
AAAGGTATCG TACAGCAGCA GGACAACCTG CTGCGTGCAA TCCAGGCACA GCAGGAACTG    300
CTGCGTCTGT CTGTATGGGG TATCCGTCAG CTGCGTGCTC GTCTGCTGGC ACTGGAAACC    360
CTGATCCAGA ACCAGCAGCT GCTGAACCTG TGGGGCTGCA AAGGTCGTCT GATCTGCTAC    420
ACCTCCGTTA AATGGAACGA AACCTGGCGT AACACCACCA ACATCAACCA GATCTGGGGT    480
AACCTGACCT GGCAGGAATG GGACCAGCAG ATCGACAACG TTTCTTCCAC CATCTACGAA    540
GAAATCCAGA AAGCTCAGGT TCAGCAGGAA CAGAACGAAA AAAAACTGCT GGAACTGGAC    600
GAATGGGCTT CTCTGTGGAA CTGGCTGGAC ATCACCAAAT GGCTGCGTAA CATCCGTCAG    660
GGCTACCAGC CGCTGTCCCT GCAGATCCCG ACCCGTCAGC AGTCTGAAGC TGAAACTCCG    720
GGTCGTACCG GTGAAGGTGG TGGTGACGAA GGCCGTCCGC GTCTGATCCC GTCTCCGCAG    780
GGTTTCCTGC CGCTGCTGTA CACCGACCTG CGTACCATCA TCCTGTGGTC CTACCACCTG    840
CTGTCTAACC TGATCTCTGG TACTCAGACT GTTATCTCTC ACCTGCGTCT GGGTCTGTGG    900
ATTCTGGGTC AGAAAATCAT CGACGCTTGC CGTATCTGCG CTGCTGTTAT CCACTACTGG    960
```

```
CTGCAGGAAC TGCAGAAATC CGCTACCTCC CTGATCGACA CCTTCGCTGT TGCAGTTGCT   1020
AACTGGACTG ACGACATCAT CCTGGGTATC CAGCGTCTGG GTCGTGGTAT CCTGAACATC   1080
CCGCGTCGTG TTCGCCAGGG CTTCGAACGC TCTCTGCTGT AATAG                   1125
```

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 373 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```
Met Ile Gly Gly Asp Met Lys Asp Ile Trp Arg Asn Glu Leu Phe Lys
 1               5                  10                  15
Tyr Lys Val Val Arg Val Lys Pro Phe Ser Val Ala Pro Thr Pro Ile
            20                  25                  30
Ala Arg Pro Val Ile Gly Thr Gly Thr His Arg Glu Lys Arg Ala Val
        35                  40                  45
Gly Leu Gly Met Leu Phe Leu Gly Val Leu Ser Ala Ala Gly Ser Thr
    50                  55                  60
Met Gly Ala Ala Ala Thr Ala Leu Thr Val Gln Thr His Ser Val Ile
65                  70                  75                  80
Lys Gly Ile Val Gln Gln Gln Asp Asn Leu Leu Arg Ala Ile Gln Ala
                85                  90                  95
Gln Gln Glu Leu Leu Arg Leu Ser Val Trp Gly Ile Arg Gln Leu Arg
            100                 105                 110
Ala Arg Leu Leu Ala Leu Glu Thr Leu Ile Gln Asn Gln Gln Leu Leu
        115                 120                 125
Asn Leu Trp Gly Cys Lys Gly Arg Leu Ile Cys Tyr Thr Ser Val Lys
    130                 135                 140
Trp Asn Glu Thr Trp Arg Asn Thr Thr Asn Ile Asn Gln Ile Trp Gly
145                 150                 155                 160
Asn Leu Thr Trp Gln Glu Trp Asp Gln Gln Ile Asp Asn Val Ser Ser
                165                 170                 175
Thr Ile Tyr Glu Glu Ile Gln Lys Ala Gln Val Gln Gln Glu Gln Asn
            180                 185                 190
Glu Lys Lys Leu Leu Glu Leu Asp Glu Trp Ala Ser Leu Trp Asn Trp
        195                 200                 205
Leu Asp Ile Thr Lys Trp Leu Arg Asn Ile Arg Gln Gly Tyr Gln Pro
    210                 215                 220
Leu Ser Leu Gln Ile Pro Thr Arg Gln Gln Ser Glu Ala Glu Thr Pro
225                 230                 235                 240
Gly Arg Thr Gly Glu Gly Gly Gly Asp Glu Gly Arg Pro Arg Leu Ile
                245                 250                 255
Pro Ser Pro Gln Gly Phe Leu Pro Leu Leu Tyr Thr Asp Leu Arg Thr
            260                 265                 270
Ile Ile Leu Trp Ser Tyr His Leu Leu Ser Asn Leu Ile Ser Gly Thr
        275                 280                 285
Gln Thr Val Ile Ser His Leu Arg Leu Gly Leu Trp Ile Leu Gly Gln
    290                 295                 300
Lys Ile Ile Asp Ala Cys Arg Ile Cys Ala Ala Val Ile His Tyr Trp
305                 310                 315                 320
Leu Gln Glu Leu Gln Lys Ser Ala Thr Ser Leu Ile Asp Thr Phe Ala
                325                 330                 335
Val Ala Val Ala Asn Trp Thr Asp Asp Ile Ile Leu Gly Ile Gln Arg
            340                 345                 350
Leu Gly Arg Gly Ile Leu Asn Ile Pro Arg Arg Val Arg Gln Gly Phe
```

```
        355                 360                 365
Glu Arg Ser Leu Leu
    370
```

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1860 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```
ATGAGTTTTG TGGTCATTAT TCCCGCGCGC TACGCGTCGA CGCGTCTGCC CGGTAAACCA      60
TTGGTTGATA TTAACGGCAA ACCCATGATT GTTCATGTTC TTGAACGCGC GCGTGAATCA     120
GGTGCCGAGC GCATCATCGT GGCAACCGAT CATGAGGATG TTGCCCGCGC CGTTGAAGCC     180
GCTGGCGGTG AAGTATGTAT GACGCGCGCC GATCATCAGT CAGGAACAGA ACGTCTGGCG     240
GAAGTTGTCG AAAAATGCGC ATTCAGCGAC GACACGGTGA TCGTTAATGT GCAGGGTGAT     300
GAACCGATGA TCCCTGCGAC AATCATTCGT CAGGTTGCTG ATAACCTCGC TCAGCGTCAG     360
GTGGGTATGA CGACTCTGGC GGTGCCAATC CACAATGCGG AAGAAGCGTT TAACCCGAAT     420
GCGGTGAAAG TGGTTCTCGA CGCTGAAGGG TATGCACTGT ACTTCTCTCG CGCCACCATT     480
CCTTGGGATC GTGATCGTTT TGCAGAAGGC CTTGAAACCG TTGGCGATAA CTTCCTGCGT     540
CATCTTGGTA TTTATGGCTA CCGTGCAGGC TTTATCCGTC GTTACGTCAA CTGGCAGCCA     600
AGTCCGTTAG AACACATCGA AATGTTAGAG CAGCTTCGTG TTCTGTGGTA CGGCGAAAAA     660
ATCCATGTTG CTGTTGCTCA GGAAGTTCCT GGCACAGGTG TGGATACCCC TGAAGATCTC     720
GACCCGTCGA CGAATTCTAT CGGTGGTGAC ATGAAAGACA TCTGGCGTAA CGAACTGTTC     780
AAATACAAAG TTGTTCGTGT TAAACCGTTC TCTGTTGCTC CGACCCCGAT CGCTCGTCCG     840
GTTATCGGTA CTGGCACCCA CCGTGAAAAA CGTGCTGTAG GTCTGGGTAT GCTGTTCCTG     900
GGCGTTCTGT CTGCAGCAGG TTCCACTATG GGTGCTGCAG CTACCGCTCT GACCGTACAG     960
ACCCACTCTG TTATCAAAGG TATCGTACAG CAGCAGGACA ACCTGCTGCG TGCAATCCAG    1020
GCACAGCAGG AACTGCTGCG TCTGTCTGTA TGGGGTATCC GTCAGCTGCG TGCTCGTCTG    1080
CTGGCACTGG AAACCCTGAT CCAGAACCAG CAGCTGCTGA ACCTGTGGGG CTGCAAAGGT    1140
CGTCTGATCT GCTACACCTC CGTTAAATGG AACGAAACCT GGCGTAACAC CACCAACATC    1200
AACCAGATCT GGGGTAACCT GACCTGGCAG GAATGGGACC AGCAGATCGA CAACGTTTCT    1260
TCCACCATCT ACGAAGAAAT CCAGAAAGCT CAGGTTCAGC AGGAACAGAA CGAAAAAAAA    1320
CTGCTGGAAC TGGACGAATG GGCTTCTCTG TGGAACTGGC TGGACATCAC CAAATGGCTG    1380
CGTAACATCC GTCAGGGCTA CCAGCCGCTG TCCCTGCAGA TCCCGACCCG TCAGCAGTCT    1440
GAAGCTGAAA CTCCGGGTCG TACCGGTGAA GGTGGTGGTG ACGAAGGCCG TCCGCGTCTG    1500
ATCCCGTCTC CGCAGGGTTT CCTGCCGCTG CTGTACACCG ACCTGCGTAC CATCATCCTG    1560
TGGTCCTACC ACCTGCTGTC TAACCTGATC TCTGGTACTC AGACTGTTAT CTCTCACCTG    1620
CGTCTGGGTC TGTGGATTCT GGGTCAGAAA ATCATCGACG CTTGCCGTAT CTGCGCTGCT    1680
GTTATCCACT ACTGGCTGCA GGAACTGCAG AAATCCGCTA CCTCCCTGAT CGACACCTTC    1740
GCTGTTGCAG TTGCTAACTG GACTGACGAC ATCATCCTGG GTATCCAGCG TCTGGGTCGT    1800
GGTATCCTGA ACATCCCGCG TCGTGTTCGC CAGGGCTTCG AACGCTCTCT GCTGTAATAG    1860
```

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 618 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```
Met Ser Phe Val Val Ile Ile Pro Ala Arg Tyr Ala Ser Thr Arg Leu
 1               5                  10                  15
```

```
Pro Gly Lys Pro Leu Val Asp Ile Asn Gly Lys Pro Met Ile Val His
            20                  25                  30
Val Leu Glu Arg Ala Arg Glu Ser Gly Ala Glu Arg Ile Ile Val Ala
        35                  40                  45
Thr Asp His Glu Asp Val Ala Arg Ala Val Glu Ala Ala Gly Gly Glu
    50                  55                  60
Val Cys Met Thr Arg Ala Asp His Gln Ser Gly Thr Glu Arg Leu Ala
65                  70                  75                  80
Glu Val Val Glu Lys Cys Ala Phe Ser Asp Asp Thr Val Ile Val Asn
                85                  90                  95
Val Gln Gly Asp Glu Pro Met Ile Pro Ala Thr Ile Ile Arg Gln Val
            100                 105                 110
Ala Asp Asn Leu Ala Gln Arg Gln Val Gly Met Thr Thr Leu Ala Val
        115                 120                 125
Pro Ile His Asn Ala Glu Glu Ala Phe Asn Pro Asn Ala Val Lys Val
    130                 135                 140
Val Leu Asp Ala Glu Gly Tyr Ala Leu Tyr Phe Ser Arg Ala Thr Ile
145                 150                 155                 160
Pro Trp Asp Arg Asp Arg Phe Ala Glu Gly Leu Glu Thr Val Gly Asp
                165                 170                 175
Asn Phe Leu Arg His Leu Gly Ile Tyr Gly Tyr Arg Ala Gly Phe Ile
            180                 185                 190
Arg Arg Tyr Val Asn Trp Gln Pro Ser Pro Leu Glu His Ile Glu Met
        195                 200                 205
Leu Glu Gln Leu Arg Val Leu Trp Tyr Gly Glu Lys Ile His Val Ala
    210                 215                 220
Val Ala Gln Glu Val Pro Gly Thr Gly Val Asp Thr Pro Glu Asp Leu
225                 230                 235                 240
Asp Pro Ser Thr Asn Ser Ile Gly Gly Asp Met Lys Asp Ile Trp Arg
                245                 250                 255
Asn Glu Leu Phe Lys Tyr Lys Val Val Arg Val Lys Pro Phe Ser Val
            260                 265                 270
Ala Pro Thr Pro Ile Ala Arg Pro Val Ile Gly Thr Gly Thr His Arg
        275                 280                 285
Glu Lys Arg Ala Val Gly Leu Gly Met Leu Phe Leu Gly Val Leu Ser
    290                 295                 300
Ala Ala Gly Ser Thr Met Gly Ala Ala Ala Thr Ala Leu Thr Val Gln
305                 310                 315                 320
Thr His Ser Val Ile Lys Gly Ile Val Gln Gln Gln Asp Asn Leu Leu
                325                 330                 335
Arg Ala Ile Gln Ala Gln Gln Glu Leu Leu Arg Leu Ser Val Trp Gly
            340                 345                 350
Ile Arg Gln Leu Arg Ala Arg Leu Leu Ala Leu Glu Thr Leu Ile Gln
        355                 360                 365
Asn Gln Gln Leu Leu Asn Leu Trp Gly Cys Lys Gly Arg Leu Ile Cys
    370                 375                 380
Tyr Thr Ser Val Lys Trp Asn Glu Thr Trp Arg Asn Thr Thr Asn Ile
385                 390                 395                 400
Asn Gln Ile Trp Gly Asn Leu Thr Trp Gln Glu Trp Asp Gln Gln Ile
                405                 410                 415
Asp Asn Val Ser Ser Thr Ile Tyr Glu Glu Ile Gln Lys Ala Gln Val
            420                 425                 430
Gln Gln Glu Gln Asn Glu Lys Lys Leu Leu Glu Leu Asp Glu Trp Ala
        435                 440                 445
Ser Leu Trp Asn Trp Leu Asp Ile Thr Lys Trp Leu Arg Asn Ile Arg
    450                 455                 460
Gln Gly Tyr Gln Pro Leu Ser Leu Gln Ile Pro Thr Arg Gln Gln Ser
465                 470                 475                 480
Glu Ala Glu Thr Pro Gly Arg Thr Gly Glu Gly Gly Gly Asp Glu Gly
                485                 490                 495
Arg Pro Arg Leu Ile Pro Ser Pro Gln Gly Phe Leu Pro Leu Leu Tyr
            500                 505                 510
```

```
Thr Asp Leu Arg Thr Ile Ile Leu Trp Ser Tyr His Leu Leu Ser Asn
        515                 520                 525
Leu Ile Ser Gly Thr Gln Thr Val Ile Ser His Leu Arg Leu Gly Leu
    530                 535                 540
Trp Ile Leu Gly Gln Lys Ile Ile Asp Ala Cys Arg Ile Cys Ala Ala
545                 550                 555                 560
Val Ile His Tyr Trp Leu Gln Glu Leu Gln Lys Ser Ala Thr Ser Leu
                565                 570                 575
Ile Asp Thr Phe Ala Val Ala Val Ala Asn Trp Thr Asp Asp Ile Ile
            580                 585                 590
Leu Gly Ile Gln Arg Leu Gly Arg Gly Ile Leu Asn Ile Pro Arg Arg
        595                 600                 605
Val Arg Gln Gly Phe Glu Arg Ser Leu Leu
    610                 615
```

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 466 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```
Met Ser Phe Val Val Ile Ile Pro Ala Arg Tyr Ala Ser Thr Arg Leu
 1               5                  10                  15
Pro Gly Lys Pro Leu Val Asp Ile Asn Gly Lys Pro Met Ile Val His
            20                  25                  30
Val Leu Glu Arg Ala Arg Glu Ser Gly Ala Glu Arg Ile Ile Val Ala
        35                  40                  45
Thr Asp His Glu Asp Val Ala Arg Ala Val Glu Ala Ala Gly Gly Glu
    50                  55                  60
Val Cys Met Thr Arg Ala Asp His Gln Ser Gly Thr Glu Arg Leu Ala
65                  70                  75                  80
Glu Val Val Glu Lys Cys Ala Phe Ser Asp Asp Thr Val Ile Val Asn
                85                  90                  95
Val Gln Gly Asp Glu Pro Met Ile Pro Ala Thr Ile Ile Arg Gln Val
            100                 105                 110
Ala Asp Asn Leu Ala Gln Arg Gln Val Gly Met Thr Thr Leu Ala Val
        115                 120                 125
Pro Ile His Asn Ala Glu Glu Ala Phe Asn Pro Asn Ala Val Lys Val
    130                 135                 140
Val Leu Asp Ala Glu Gly Tyr Ala Leu Tyr Phe Ser Arg Ala Thr Ile
145                 150                 155                 160
Pro Trp Asp Arg Asp Arg Phe Ala Glu Gly Leu Glu Thr Val Gly Asp
                165                 170                 175
Asn Phe Leu Arg His Leu Gly Ile Tyr Gly Tyr Arg Ala Gly Phe Ile
            180                 185                 190
Arg Arg Tyr Val Asn Trp Gln Pro Ser Pro Leu Glu His Ile Glu Met
        195                 200                 205
Leu Glu Gln Leu Arg Val Leu Trp Tyr Gly Glu Lys Ile His Val Ala
    210                 215                 220
Val Ala Gln Glu Val Pro Gly Thr Gly Val Asp Thr Pro Glu Asp Leu
225                 230                 235                 240
Asp Pro Ser Thr Asn Ser Met Glu Gly Glu Leu Thr Cys Asn Ser Thr
                245                 250                 255
Val Thr Ser Ile Ile Ala Asn Ile Asp Ser Asp Gly Asn Gln Thr Asn
            260                 265                 270
Ile Thr Phe Ser Ala Glu Val Ala Glu Leu Tyr Arg Leu Glu Leu Gly
        275                 280                 285
```

```
Asp Tyr Lys Leu Ile Glu Val Thr Pro Ile Gly Phe Ala Pro Thr Lys
290                 295                 300
Glu Lys Arg Tyr Ser Ser Ala Pro Val Arg Asn Lys Arg Gly Val Phe
305                 310                 315                 320
Val Leu Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser Ala Met Gly
                325                 330                 335
Ala Ala Ser Leu Thr Leu Ser Ala Gln Ser Arg Thr Leu Leu Ala Gly
            340                 345                 350
Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg Gln Gln
        355                 360                 365
Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln Ala Arg
370                 375                 380
Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln Leu Asn Ser
385                 390                 395                 400
Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Thr Val Pro Trp Val
                405                 410                 415
Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn Met Thr Trp Gln Glu Trp
            420                 425                 430
Glu Lys Arg Val His Tyr Leu Glu Ala Asn Ile Ser Gln Ser Leu Glu
        435                 440                 445
Gln Ala Gln Ile Gln Gln Glu Lys Asn Met Tyr Glu Leu Gln Lys Leu
450                 455                 460
Asn Ser
465
```

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 491 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```
Met Ser Phe Val Val Ile Ile Pro Ala Arg Tyr Ala Ser Thr Arg Leu
 1                5                  10                  15
Pro Gly Lys Pro Leu Val Asp Ile Asn Gly Lys Pro Met Ile Val His
            20                  25                  30
Val Leu Glu Arg Ala Arg Glu Ser Gly Ala Glu Arg Ile Ile Val Ala
        35                  40                  45
Thr Asp His Glu Asp Val Ala Arg Ala Val Glu Ala Ala Gly Gly Glu
    50                  55                  60
Val Cys Met Thr Arg Ala Asp His Gln Ser Gly Thr Glu Arg Leu Ala
65                  70                  75                  80
Glu Val Val Glu Lys Cys Ala Phe Ser Asp Asp Thr Val Ile Val Asn
                85                  90                  95
Val Gln Gly Asp Glu Pro Met Ile Pro Ala Thr Ile Ile Arg Gln Val
            100                 105                 110
Ala Asp Asn Leu Ala Gln Arg Gln Val Gly Met Ala Thr Leu Ala Val
        115                 120                 125
Pro Ile His Asn Ala Glu Glu Ala Phe Asn Pro Asn Ala Val Lys Val
    130                 135                 140
Val Leu Asp Ala Glu Gly Tyr Ala Leu Tyr Phe Ser Arg Ala Thr Ile
145                 150                 155                 160
Pro Trp Asp Arg Asp Arg Phe Ala Glu Gly Leu Glu Thr Val Gly Asp
                165                 170                 175
Asn Phe Leu Arg His Leu Gly Ile Tyr Gly Tyr Arg Ala Gly Phe Ile
            180                 185                 190
Arg Arg Tyr Val Asn Trp Gln Pro Ser Pro Leu Glu His Ile Glu Met
        195                 200                 205
```

```
Leu Glu Gln Leu Arg Val Leu Trp Tyr Gly Glu Lys Ile His Val Ala
    210                 215                 220
Val Ala Gln Glu Val Pro Gly Thr Gly Val Asp Thr Pro Glu Asp Pro
225                 230                 235                 240
Ser Thr Ala Leu Met Lys Ile Pro Gly Asp Pro Gly Gly Gly Asp Met
                245                 250                 255
Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
            260                 265                 270
Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
        275                 280                 285
Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
    290                 295                 300
Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val
305                 310                 315                 320
Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
                325                 330                 335
Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
            340                 345                 350
Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Leu
        355                 360                 365
Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
    370                 375                 380
Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
385                 390                 395                 400
Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
                405                 410                 415
Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
            420                 425                 430
Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Val
        435                 440                 445
Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His Leu
    450                 455                 460
Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Lys Lys Ala
465                 470                 475                 480
Ala Asn Val Thr Val Thr Val Pro Phe Val Trp
                485                 490
```

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 651 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```
ATGATCGGTG GTGACATGAA AGACATCTGG CGTAACGAAC TGTTCAAATA CAAAGTTGTT     60
CGTGTTAAAC CGTTCTCTGT TGCTCCGACC CCGATCGCTC GTCCGGTTAT CGGTACTGGC    120
ACCCACCGTG AAAAACGTGC TGTAGGTCTG GGTATGCTGT TCCTGGGCGT TCTGTCTGCA    180
GCAGGTTCCA CTATGGGTGC TGCAGCTACC GCTCTGACCG TACAGACCCA CTCTGTTATC    240
AAAGGTATCG TACAGCAGCA GGACAACCTG CTGCGTGCAA TCCAGGCACA GCAGGAACTG    300
CTGCGTCTGT CTGTATGGGG TATCCGTCAG CTGCGTGCTC GTCTGCTGGC ACTGGAAACC    360
CTGATCCAGA ACCAGCAGCT GCTGAACCTG TGGGGCTGCA AAGGTCGTCT GATCTGCTAC    420
ACCTCCGTTA AATGGAACGA AACCTGGCGT AACACCACCA ACATCAACCA GATCTGGGGT    480
AACCTGACCT GGCAGGAATG GGACCAGCAG ATCGACAACG TTTCTTCCAC CATCTACGAA    540
GAAATCCAGA AAGCTCAGGT TCAGCAGGAA CAGAACGAAA AAAAACTGCT GGAACTGGAC    600
GAATGGGCTT CTCTGTGGAA CTGGCTGGAC ATCACCAAAT GGCTGTAATA G             651
```

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 215 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```
Met Ile Gly Gly Asp Met Lys Asp Ile Trp Arg Asn Glu Leu Phe Lys
 1               5                  10                  15
Tyr Lys Val Val Arg Val Lys Pro Phe Ser Val Ala Pro Thr Pro Ile
            20                  25                  30
Ala Arg Pro Val Ile Gly Thr Gly Thr His Arg Glu Lys Arg Ala Val
        35                  40                  45
Gly Leu Gly Met Leu Phe Leu Gly Val Leu Ser Ala Ala Gly Ser Thr
    50                  55                  60
Met Gly Ala Ala Ala Thr Ala Leu Thr Val Gln Thr His Ser Val Ile
65                  70                  75                  80
Lys Gly Ile Val Gln Gln Gln Asp Asn Leu Leu Arg Ala Ile Gln Ala
                85                  90                  95
Gln Gln Glu Leu Leu Arg Leu Ser Val Trp Gly Ile Arg Gln Leu Arg
            100                 105                 110
Ala Arg Leu Leu Ala Leu Glu Thr Leu Ile Gln Asn Gln Gln Leu Leu
        115                 120                 125
Asn Leu Trp Gly Cys Lys Gly Arg Leu Ile Cys Tyr Thr Ser Val Lys
    130                 135                 140
Trp Asn Glu Thr Trp Arg Asn Thr Thr Asn Ile Asn Gln Ile Trp Gly
145                 150                 155                 160
Asn Leu Thr Trp Gln Glu Trp Asp Gln Gln Ile Asp Asn Val Ser Ser
                165                 170                 175
Thr Ile Tyr Glu Glu Ile Gln Lys Ala Gln Val Gln Gln Glu Gln Asn
            180                 185                 190
Glu Lys Lys Leu Leu Glu Leu Asp Glu Trp Ala Ser Leu Trp Asn Trp
        195                 200                 205
Leu Asp Ile Thr Lys Trp Leu
    210                 215
```

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```
ATGAGTTTTG TGGTCATTAT TCCCGCGCGC TACGCGTCGA CGCGTCTGCC CGGTAAACCA     60
TTGGTTGATA TTAACGGCAA ACCCATGATT GTTCATGTTC TTGAACGCGC GCGTGAATCA    120
GGTGCCGAGC GCATCATCGT GGCAACCGAT CATGAGGATG TTGCCCGCGC CGTTGAAGCC    180
GCTGGCGGTG AAGTATGTAT GACGCGCGCC GATCATCAGT CAGGAACAGA ACGTCTGGCG    240
GAAGTTGTCG AAAAATGCGC ATTCAGCGAC GACACGGTGA TCGTTAATGT GCAGGGTGAT    300
GAACCGATGA TCCCTGCGAC AATCATTCGT CAGGTTGCTG ATAACCTCGC TCAGCGTCAG    360
GTGGGTATGA CGACTCTGGC GGTGCCAATC CACAATGCGG AAGAAGCGTT TAACCCGAAT    420
GCGGTGAAAG TGGTTCTCGA CGCTGAAGGG TATGCACTGT ACTTCTCTCG CGCCACCATT    480
CCTTGGGATC GTGATCGTTT TGCAGAAGGC CTTGAAACCG TTGGCGATAA CTTCCTGCGT    540
CATCTTGGTA TTTATGGCTA CCGTGCAGGC TTTATCCGTC GTTACGTCAA CTGGCAGCCA    600
AGTCCGTTAG AACACATCGA AATGTTAGAG CAGCTTCGTG TTCTGTGGTA CGGCGAAAAA    660
ATCCATGTTG CTGTTGCTCA GGAAGTTCCT GGCACAGGTG TGGATACCCC TGAAGATCTC    720
GACCCGTCGA CGAATTCTAT CGGTGGTGAC ATGAAAGACA TCTGGCGTAA CGAACTGTTC    780
```

```
AAATACAAAG TTGTTCGTGT TAAACCGTTC TCTGTTGCTC CGACCCCGAT CGCTCGTCCG    840
GTTATCGGTA CTGGCACCCA CCGTGAAAAA CGTGCTGTAG GTCTGGGTAT GCTGTTCCTG    900
GGCGTTCTGT CTGCAGCAGG TTCCACTATG GGTGCTGCAG CTACCGCTCT GACCGTACAG    960
ACCCACTCTG TTATCAAAGG TATCGTACAG CAGCAGGACA ACCTGCTGCG TGCAATCCAG   1020
GCACAGCAGG AACTGCTGCG TCTGTCTGTA TGGGGTATCC GTCAGCTGCG TGCTCGTCTG   1080
CTGGCACTGG AAACCCTGAT CCAGAACCAG CAGCTGCTGA ACCTGTGGGG CTGCAAAGGT   1140
CGTCTGATCT GCTACACCTC CGTTAAATGG AACGAAACCT GGCGTAACAC CACCAACATC   1200
AACCAGATCT GGGGTAACCT GACCTGGCAG GAATGGGACC AGCAGATCGA CAACGTTTCT   1260
TCCACCATCT ACGAAGAAAT CCAGAAAGCT CAGGTTCAGC AGGAACAGAA CGAAAAAAAA   1320
CTGCTGGAAC TGGACGAATG GGCTTCTCTG TGGAACTGGC TGGACATCAC CAAATGGCTG   1380
TAATAG                                                              1386
```

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 460 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```
Met Ser Phe Val Val Ile Ile Pro Ala Arg Tyr Ala Ser Thr Arg Leu
 1               5                  10                  15
Pro Gly Lys Pro Leu Val Asp Ile Asn Gly Lys Pro Met Ile Val His
            20                  25                  30
Val Leu Glu Arg Ala Arg Glu Ser Gly Ala Glu Arg Ile Ile Val Ala
        35                  40                  45
Thr Asp His Glu Asp Val Ala Arg Ala Val Glu Ala Ala Gly Gly Glu
    50                  55                  60
Val Cys Met Thr Arg Ala Asp His Gln Ser Gly Thr Glu Arg Leu Ala
65                  70                  75                  80
Glu Val Val Glu Lys Cys Ala Phe Ser Asp Asp Thr Val Ile Val Asn
                85                  90                  95
Val Gln Gly Asp Glu Pro Met Ile Pro Ala Thr Ile Ile Arg Gln Val
            100                 105                 110
Ala Asp Asn Leu Ala Gln Arg Gln Val Gly Met Thr Thr Leu Ala Val
        115                 120                 125
Pro Ile His Asn Ala Glu Glu Ala Phe Asn Pro Asn Ala Val Lys Val
    130                 135                 140
Val Leu Asp Ala Glu Gly Tyr Ala Leu Tyr Phe Ser Arg Ala Thr Ile
145                 150                 155                 160
Pro Trp Asp Arg Asp Arg Phe Ala Glu Gly Leu Glu Thr Val Gly Asp
                165                 170                 175
Asn Phe Leu Arg His Leu Gly Ile Tyr Gly Tyr Arg Ala Gly Phe Ile
            180                 185                 190
Arg Arg Tyr Val Asn Trp Gln Pro Ser Pro Leu Glu His Ile Glu Met
        195                 200                 205
Leu Glu Gln Leu Arg Val Leu Trp Tyr Gly Glu Lys Ile His Val Ala
    210                 215                 220
Val Ala Gln Glu Val Pro Gly Thr Gly Val Asp Thr Pro Glu Asp Leu
225                 230                 235                 240
Asp Pro Ser Thr Asn Ser Ile Gly Gly Asp Met Lys Asp Ile Trp Arg
                245                 250                 255
Asn Glu Leu Phe Lys Tyr Lys Val Val Arg Val Lys Pro Phe Ser Val
            260                 265                 270
Ala Pro Thr Pro Ile Ala Arg Pro Val Ile Gly Thr Gly Thr His Arg
        275                 280                 285
Glu Lys Arg Ala Val Gly Leu Gly Met Leu Phe Leu Gly Val Leu Ser
```

```
    290                 295                 300
Ala Ala Gly Ser Thr Met Gly Ala Ala Ala Thr Ala Leu Thr Val Gln
305                 310                 315                 320
Thr His Ser Val Ile Lys Gly Ile Val Gln Gln Gln Asp Asn Leu Leu
                325                 330                 335
Arg Ala Ile Gln Ala Gln Gln Glu Leu Leu Arg Leu Ser Val Trp Gly
            340                 345                 350
Ile Arg Gln Leu Arg Ala Arg Leu Leu Ala Leu Glu Thr Leu Ile Gln
        355                 360                 365
Asn Gln Gln Leu Leu Asn Leu Trp Gly Cys Lys Gly Arg Leu Ile Cys
    370                 375                 380
Tyr Thr Ser Val Lys Trp Asn Glu Thr Trp Arg Asn Thr Thr Asn Ile
385                 390                 395                 400
Asn Gln Ile Trp Gly Asn Leu Thr Trp Gln Glu Trp Asp Gln Gln Ile
                405                 410                 415
Asp Asn Val Ser Ser Thr Ile Tyr Glu Glu Ile Gln Lys Ala Gln Val
            420                 425                 430
Gln Gln Glu Gln Asn Glu Lys Lys Leu Leu Glu Leu Asp Glu Trp Ala
        435                 440                 445
Ser Leu Trp Asn Trp Leu Asp Ile Thr Lys Trp Leu
    450                 455                 460
```

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 873 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```
Met Ile Val Thr Met Arg Ala Met Gly Lys Arg Asn Arg Lys Leu Gly
 1                5                  10                  15
Ile Leu Tyr Ile Val Met Ala Leu Ile Ile Pro Cys Leu Ser Ser Ser
            20                  25                  30
Gln Leu Tyr Ala Thr Val Tyr Ala Gly Val Pro Val Trp Glu Asp Ala
        35                  40                  45
Ala Pro Val Leu Phe Cys Ala Ser Asp Ala Asn Leu Thr Ser Thr Glu
    50                  55                  60
Lys His Asn Val Trp Ala Ser Gln Ala Cys Val Pro Thr Asp Pro Thr
65                  70                  75                  80
Pro His Glu Tyr Leu Leu Thr Asn Val Thr Asp Asn Phe Asn Ile Trp
                85                  90                  95
Glu Asn Tyr Met Val Glu Gln Met Gln Glu Asp Ile Ile Ser Leu Trp
            100                 105                 110
Asp Gln Ser Leu Lys Pro Cys Ile Gln Met Thr Phe Met Cys Ile Gln
        115                 120                 125
Met Asn Cys Thr Asp Ile Lys Asn Asn Asn Thr Ser Gly Thr Glu Asn
    130                 135                 140
Arg Thr Ser Ser Ser Glu Asn Pro Met Lys Thr Cys Glu Phe Asn Ile
145                 150                 155                 160
Thr Thr Val Leu Lys Asp Lys Lys Glu Lys Lys Gln Ala Leu Phe Tyr
                165                 170                 175
Val Ser Asp Leu Thr Lys Leu Ala Asp Asn Asn Thr Thr Asn Thr Met
            180                 185                 190
Tyr Thr Leu Ile Asn Cys Asn Ser Thr Thr Ile Lys Gln Ala Cys Pro
        195                 200                 205
Lys Val Ser Phe Glu Pro Ile Pro Ile Tyr Tyr Cys Ala Pro Ala Gly
```

```
    210                 215                 220
Tyr Ala Ile Phe Lys Cys Asn Ser Ala Glu Phe Asn Gly Thr Gly Lys
225                 230                 235                 240
Cys Ser Asn Ile Ser Val Val Thr Cys Thr His Gly Ile Lys Pro Thr
                245                 250                 255
Val Ser Thr Gln Leu Ile Leu Asn Gly Thr Leu Ser Lys Glu Lys Ile
            260                 265                 270
Arg Ile Met Gly Lys Asn Ile Ser Asp Ser Gly Lys Asn Ile Ile Val
        275                 280                 285
Thr Leu Ser Ser Asp Ile Glu Ile Thr Cys Val Arg Pro Gly Asn Asn
    290                 295                 300
Gln Thr Val Gln Glu Met Lys Ile Gly Pro Met Ala Trp Tyr Ser Met
305                 310                 315                 320
Ala Leu Gly Thr Gly Ser Asn Arg Ser Arg Val Ala Tyr Cys Gln Tyr
                325                 330                 335
Asn Thr Thr Glu Trp Glu Lys Ala Leu Lys Asn Thr Ala Glu Arg Tyr
            340                 345                 350
Leu Glu Leu Ile Asn Asn Thr Glu Gly Asn Thr Thr Met Ile Phe Asn
        355                 360                 365
Arg Ser Gln Asp Gly Ser Asp Val Glu Val Thr His Leu His Phe Asn
    370                 375                 380
Cys His Gly Glu Phe Phe Tyr Cys Asn Thr Ser Glu Met Phe Asn Tyr
385                 390                 395                 400
Thr Phe Leu Cys Asn Gly Thr Asn Cys Asn Asn Thr Gln Ser Ile Asn
                405                 410                 415
Ser Ala Asn Gly Met Ile Pro Cys Lys Leu Lys Gln Val Val Arg Ser
            420                 425                 430
Trp Met Arg Gly Gly Ser Gly Leu Tyr Ala Pro Pro Ile Pro Gly Asn
        435                 440                 445
Leu Thr Cys Ile Ser His Ile Thr Gly Met Ile Leu Gln Met Asp Ala
    450                 455                 460
Pro Trp Asn Lys Thr Glu Asn Thr Phe Arg Pro Ile Gly Gly Asp Met
465                 470                 475                 480
Lys Asp Ile Trp Arg Asn Glu Leu Phe Lys Tyr Lys Val Val Arg Val
                485                 490                 495
Lys Pro Phe Ser Val Ala Pro Thr Pro Ile Ala Arg Pro Val Ile Gly
            500                 505                 510
Thr Gly Thr His Arg Glu Lys Arg Ala Val Gly Leu Gly Met Leu Phe
        515                 520                 525
Leu Gly Val Leu Ser Ala Ala Gly Ser Thr Met Gly Ala Ala Ala Thr
    530                 535                 540
Ala Leu Thr Val Gln Thr His Ser Val Ile Lys Gly Ile Val Gln Gln
545                 550                 555                 560
Gln Asp Asn Leu Leu Arg Ala Ile Gln Ala Gln Gln Glu Leu Leu Arg
                565                 570                 575
Leu Ser Val Trp Gly Ile Arg Gln Leu Arg Ala Arg Leu Leu Ala Leu
            580                 585                 590
Glu Thr Leu Ile Gln Asn Gln Gln Leu Leu Asn Leu Trp Gly Cys Lys
        595                 600                 605
Gly Arg Leu Ile Cys Tyr Thr Ser Val Lys Trp Asn Glu Thr Trp Arg
    610                 615                 620
Asn Thr Thr Asn Ile Asn Gln Ile Trp Gly Asn Leu Thr Trp Gln Glu
625                 630                 635                 640
Trp Asp Gln Gln Ile Asp Asn Val Ser Ser Thr Ile Tyr Glu Glu Ile
                645                 650                 655
Gln Lys Ala Gln Val Gln Gln Glu Gln Asn Glu Lys Lys Leu Leu Glu
            660                 665                 670
Leu Asp Glu Trp Ala Ser Leu Trp Asn Trp Leu Asp Ile Thr Lys Trp
        675                 680                 685
Leu Trp Tyr Ile Lys Ile Ala Ile Ile Ile Val Gly Ala Leu Ile Gly
    690                 695                 700
Val Arg Ile Val Met Ile Val Leu Asn Leu Val Arg Asn Ile Arg Gln
```

```
705                 710                 715                 720
Gly Tyr Gln Pro Leu Ser Leu Gln Ile Pro Thr Arg Gln Gln Ser Glu
                725                 730                 735
Ala Glu Thr Pro Gly Arg Thr Gly Glu Gly Gly Gly Asp Glu Gly Arg
            740                 745                 750
Pro Arg Leu Ile Pro Ser Pro Gln Gly Phe Leu Pro Leu Leu Tyr Thr
        755                 760                 765
Asp Leu Arg Thr Ile Ile Leu Trp Ser Tyr His Leu Leu Ser Asn Leu
    770                 775                 780
Ile Ser Gly Thr Gln Thr Val Ile Ser His Leu Arg Leu Gly Leu Trp
785                 790                 795                 800
Ile Leu Gly Gln Lys Ile Ile Asp Ala Cys Arg Ile Cys Ala Ala Val
                805                 810                 815
Ile His Tyr Trp Leu Gln Glu Leu Gln Lys Ser Ala Thr Ser Leu Ile
            820                 825                 830
Asp Thr Phe Ala Val Ala Val Ala Asn Trp Thr Asp Asp Ile Ile Leu
        835                 840                 845
Gly Ile Gln Arg Leu Gly Arg Gly Ile Leu Asn Ile Pro Arg Arg Val
    850                 855                 860
Arg Gln Gly Phe Glu Arg Ser Leu Leu
865                 870
```

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

YCTYTAGAGA GTGTCCCATT 20

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GTGCTWCCTG CTGCACTTA 19

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

AAGTTGCTCA AGAGGTGGTA 20

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CCTTAGAGGC ACTTGAGGT 19

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CCARAGCAGT AAGTAACGC 19

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

RTTAAYTAAT TGTAACTCCA CAA 23

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GAMTYTATGC ACCTCCCATC 20

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GACATAACTA AATGGTTGTG G 21

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATACTTGARA GRTTAAGRAG AAT 23

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ATGCCATGTG TACAAGTAAC 20

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

ATACACTATT GTGCTCCARC 20

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

AGTTCTCCAT ATATCTTTCA TR 22

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AACATAACTG GAATGATYCT AC 22

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CTGAGRTCCG TGTACAAC 18

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ATTAGGCAGG GATATCAACC 20

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CCTACTCCAG GTGCRCAT 18

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAWCACAAGC CTGYGTTCC 19

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

ATGTCTTCVT GCATTTGKTC 20

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

AATGGGACAC TCTCTARAGR 20

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTAACTGTCA TGGAGAATTC TT 22

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AAGAATTCTC CATGACAGTT AA 22

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TAAGTGCAGC AGGWAGCAC 19

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CCACAACCAT TTAGTTATGT C 21

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TACCACCTCT TGAGCAACTT 20

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CYTGTCTAAT YCTYCTTGG 19

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TGGCCTGGTA CAGCATGGG 19

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTACGAATTC CATGGAAGGG GAGTTGACCT GC 32

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TATTGGATCC TTATCAGCTA TTTAGTTTTT GTAG 34

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2214 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

ATGAGTTTTG TGGTCATTAT TCCCGCGCGC TACGCGTCGA CGCGTCTGCC 50
CGGTAAACCA TTGGTTGATA TTAACGGCAA ACCCATGATT GTTCATGTTC 100
TTGAACGCGC GCGTGAATCA GGTGCCGAGC GCATCATCGT GGCAACCGAT 150
CATGAGGATG TTGCCCGCGC CGTTGAAGCC GCTGGCGGTG AAGTATGTAT 200
GACGCGCGCC GATCATCAGT CAGGAACAGA ACGTCTGGCG GAAGTTGTCG 250
AAAAATGCGC ATTCAGCGAC GACACGGTGA TCGTTAATGT GCAGGGTGAT 300
GAACCGATGA TCCCTGCGAC AATCATTCGT CAGGTTGCTG ATAACCTCGC 350
TCAGCGTCAG GTGGGTATGG CGACTCTGGC GGTGCCAATC CACAATGCGG 400
AAGAAGCGTT TAACCCGAAT GCGGTGAAAG TGGTTCTCGA CGCTGAAGGG 450
TATGCACTGT ACTTCTCTCG CGCCACCATT CCTTGGGATC GTGATCGTTT 500
TGCAGAAGGC CTTGAAACCG TTGGCGATAA CTTCCTGCGT CATCTTGGTA 550
TTTATGGCTA CCGTGCAGGC TTTATCCGTC GTTACGTCAA CTGGCAGCCA 600
AGTCCGTTAG AACACATCGA AATGTTAGAG CAGCTTCGTG TTCTGTGGTA 650
CGGCGAAAAA ATCCATGTTG CTGTTGCTCA GGAAGTTCCT GGCACAGGTG 700
TGGATACCCC TGAAGATCCG TCGACAGCCC TTATGAAGAT CCCCGGCGAC 750
CCGGGTGGTG GTGACATGCG TGACAACTGG CGTTCTGAAC TGTACAAATA 800
CAAAGTTGTT AAAATCGAAC CGCTGGGTGT TGCTCCGACT AAAGCTAAAC 850
GTCGTGTTGT TCAGCGTGAA AAACGCGCCG TTGGTATCGG TGCACTGTTC 900
CTGGGTTTCC TGGGTGCTGC TGGTTCTACC ATGGGTGCTG CTTCTATGAC 950
CCTGACTGTT CAGGCCCGTC AGCTTCTGTC TGGTATCGTT CAGCAGCAGA 1000
ACAATCTGCT GCGTGCTATC GAAGCTCAGC AGCATCTGCT GCAACTGACC 1050
GTTTGGGGTA TCAAACAGCT TCAGGCTCGT ATCCTGGCTG TTGAACGTTA 1100
CCTGAAAGAC CAGCAGCTGC TGGGTATCTG GGGTTGCTCT GGTAAACTGA 1150
TCTGCACTAC TGCTGTTCCG TGGAACGCTT CTTGGTCTAA CAAATCTCTG 1200
GAACAGATCT GGAACAACAT GACTTGGATG GAATGGGACC GTGAAATCAA 1250
CAACTACACA AGCTTGATCC ACTCTCTGAT CGAAGAAAGC CAGAACCAGC 1300
AGGAAAAAAA CGAACAGGAA CTTCTAGAAC TGGACAAATG GGTTAACCGT 1350
GTTCGTCAGG GTTACTCTCC GCTGTCTTTC CAGACCCATC TGCCGATCCC 1400
GCGTGGTCCG GACCGTCCGG AAGGTATCGA AGAAGAAGGC GGCGAACGTG 1450
ACCGTGACCG TTCCATTCGT CTGGTAATCG GTGGTGACAT GAAAGACATC 1500
TGGCGTAACG AACTGTTCAA ATACAAAGTT GTTCGTGTTA AACCGTTCTC 1550
TGTTGCTCCG ACCCCGATCG CTCGTCCGGT TATCGGTACT GGCACCCACC 1600
GTGAAAAACG TGCTGTAGGT CTGGGTATGC TGTTCCTGGG CGTTCTGTCT 1650
GCAGCAGGTT CCACTATGGG TGCTGCAGCT ACCGCTCTGA CCGTACAGAC 1700
CCACTCTGTT ATCAAAGGTA TCGTACAGCA GCAGGACAAC CTGCTGCGTG 1750

```
CAATCCAGGC ACAGCAGGAA CTGCTGCGTC TGTCTGTATG GGGTATCCGT          1800
CAGCTGCGTG CTCGTCTGCT GGCACTGGAA ACCCTGATCC AGAACCAGCA          1850
GCTGCTGAAC CTGTGGGGCT GCAAAGGTCG TCTGATCTGC TACACCTCCG          1900
TTAAATGGAA CGAAACCTGG CGTAACACCA CCAACATCAA CCAGATCTGG          1950
GGTAACCTGA CCTGGCAGGA ATGGGACCAG CAGATCGACA ACGTTTCTTC          2000
CACCATCTAC GAAGAAATCC AGAAAGCTCA GGTTCAGCAG GAACAGAACG          2050
AAAAAAAACT GCTGGAACTG GACGAATGGG CTTCTCTGTG GAACTGGCTG          2100
GACATCACCA AATGGCTGCG TAACATCCGT CAGGGCTACC AGCCGCTGTC          2150
CCTGCAGATC CCGACCCGTC AGCAGTCTGA AGCTGAAACT CCGGGTCGTA          2200
CCGGTGAATA ATAG                                                2214
```

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 736 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```
MSFVVIIPAR YASTRLPGKP LVDINGKPMI VHVLERARES GAERIIVATD          50
HEDVARAVEA AGGEVCMTRA DHQSGTERLA EVVEKCAFSD DTVIVNVQGD         100
EPMIPATIIR QVADNLAQRQ VGMATLAVPI HNAEEAFNPN AVKVVLDAEG         150
YALYFSRATI PWDRDRFAEG LETVGDNFLR HLGIYGYRAG FIRRYVNWQP         200
SPLEHIEMLE QLRVLWYGEK IHVAVAQEVP GTGVDTPEDP STALMKIPGD         250
PGGGDMRDNW RSELYKYKVV KIEPLGVAPT KAKRRVVQRE KRAVGIGALF         300
LGFLGAAGST MGAASMTLTV QARQLLSGIV QQQNNLLRAI EAQQHLLQLT         350
VWGIKQLQAR ILAVERYLKD QQLLGIWGCS GKLICTTAVP WNASWSNKSL         400
EQIWNNMTWM EWDREINNYT SLIHSLIEES QNQQEKNEQE LLELDKWVNR         450
VRQGYSPLSF QTHLPIPRGP DRPEGIEEEG GERDRDRSIR LVIGGDMKDI         500
WRNELFKYKV VRVKPFSVAP TPIARPVIGT GTHREKRAVG LGMLFLGVLS         550
AAGSTMGAAA TALTVQTHSV IKGIVQQQDN LLRAIQAQQE LLRLSVWGIR         600
QLRARLLALE TLIQNQQLLN LWGCKGRLIC YTSVKWNETW RNTTNINQIW         650
GNLTWQEWDQ QIDNVSSTIY EEIQKAQVQQ EQNEKKLLEL DEWASLWNWL         700
DITKWLRNIR QGYQPLSLQI PTRQQSEAET PGRTGE                        736
```

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```
ATGAGTTTTG TGGTCATTAT TCCCGCGCGC TACGCGTCGA CGCGTCTGCC           50
CGGTAAACCA TTGGTTGATA TTAACGGCAA ACCCATGATT GTTCATGTTC          100
TTGAACGCGC GCGTGAATCA GGTGCCGAGC GCATCATCGT GGCAACCGAT          150
CATGAGGATG TTGCCCGCGC CGTTGAAGCC GCTGGCGGTG AAGTATGTAT          200
GACGCGCGCC GATCATCAGT CAGGAACAGA ACGTCTGGCG GAAGTTGTCG          250
AAAAATGCGC ATTCAGCGAC GACACGGTGA TCGTTAATGT GCAGGGTGAT          300
GAACCGATGA TCCCTGCGAC AATCATTCGT CAGGTTGCTG ATAACCTCGC          350
TCAGCGTCAG GTGGGTATGG CGACTCTGGC GGTGCCAATC CACAATGCGG          400
AAGAAGCGTT TAACCCGAAT GCGGTGAAAG TGGTTCTCGA CGCTGAAGGG          450
TATGCACTGT ACTTCTCTCG CGCCACCATT CCTTGGGATC GTGATCGTTT          500
TGCAGAAGGC CTTGAAACCG TTGGCGATAA CTTCCTGCGT CATCTTGGTA          550
```

TTTATGGCTA CCGTGCAGGC TTTATCCGTC GTTACGTCAA CTGGCAGCCA 600
AGTCCGTTAG AACACATCGA AATGTTAGAG CAGCTTCGTG TTCTGTGGTA 650
CGGCGAAAAA ATCCATGTTG CTGTTGCTCA GGAAGTTCCT GGCACAGGTG 700
TGGATACCCC TGAAGATCCG TCGACAGCCC TTATGAAGAT CCCCGGCGAC 750
CCGGGTGGTG GTGACATGCG TGACAACTGG CGTTCTGAAC TGTACAAATA 800
CAAAGTTGTT AAAATCGAAC CGCTGGGTGT TGCTCCGACT AAAGCTAAAC 850
GTCGTGTTGT TCAGCGTGAA AAACGCGCCG TTGGTATCGG TGCACTGTTC 900
CTGGGTTTCC TGGGTGCTGC TGGTTCTACC ATGGGTGCTG CTTCTATGAC 950
CCTGACTGTT CAGGCCCGTC AGCTTCTGTC TGGTATCGTT CAGCAGCAGA 1000
ACAATCTGCT GCGTGCTATC GAAGCTCAGC AGCATCTGCT GCAACTGACC 1050
GTTTGGGGTA TCAAACAGCT TCAGGCTCGT ATCCTGGCTG TTGAACGTTA 1100
CCTGAAAGAC CAGCAGCTGC TGGGTATCTG GGGTTGCTCT GGTAAACTGA 1150
TCTGCACTAC TGCTGTTCCG TGGAACGCTT CTTGGTCTAA CAAATCTCTG 1200
GAACAGATCT GGAACAACAT GACTTGGATG GAATGGGACC GTGAAATCAA 1250
CAACTACACA AGCTTGATCC ACTCTCTGAT CGAAGAAAGC CAGAACCAGC 1300
AGGAAAAAAA CGAACAGGAA CTTCTAGAAC TGGACAAATG GGTTAACCGT 1350
GTTCGTCAGG GTTACTCTCC GCTGTCTTTC CAGACCCATC TGCCGATCCC 1400
GCGTGGTCCG GACCGTCCGG AAGGTATCGA AGAAGAAGGC GGCGAACGTG 1450
ACCGTGACCG TTCCATTCGT CTGGTAATCG GTGGTGACAT GAAAGACATC 1500
TGGCGTAACG AACTGTTCAA ATACAAAGTT GTTCGTGTTA AACCGTTCTC 1550
TGTTGCTCCG ACCCCGATCG CTCGTCCGGT TATCGGTACT GGCACCCACC 1600
GTGAAAAACG TGCTGTAGGT CTGGGTATGC TGTTCCTGGG CGTTCTGTCT 1650
GCAGCAGGTT CCACTATGGG TGCTGCAGCT ACCGCTCTGA CCGTACAGAC 1700
CCACTCTGTT ATCAAAGGTA TCGTACAGCA GCAGGACAAC CTGCTGCGTG 1750
CAATCCAGGC ACAGCAGGAA CTGCTGCGTC TGTCTGTATG GGGTATCCGT 1800
CAGCTGCGTG CTCGTCTGCT GGCACTGGAA ACCCTGATCC AGAACCAGCA 1850
GCTGCTGAAC CTGTGGGGCT GCAAAGGTCG TCTGATCTGC TACACCTCCG 1900
TTAAATGGAA CGAAACCTGG CGTAACACCA CCAACATCAA CCAGATCTGG 1950
GGTAACCTGA CCTGGCAGGA ATGGGACCAG CAGATCGACA ACGTTTCTTC 2000
CACCATCTAC GAAGAAATCC AGAAAGCTCA GGTTCAGCAG GAACAGAACG 2050
AAAAAAAACT GCTGGAACTG GACGAATGGG CTTCTCTGTG GAACTGGCTG 2100
GACATCACCA AATGGCTGTA ATAG 2124

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 706 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

MSFVVIIPAR YASTRLPGKP LVDINGKPMI VHVLERARES GAERIIVATD 50
HEDVARAVEA AGGEVCMTRA DHQSGTERLA EVVEKCAFSD DTVIVNVQGD 100
EPMIPATIIR QVADNLAQRQ VGMATLAVPI HNAEEAFNPN AVKVVLDAEG 150
YALYFSRATI PWDRDRFAEG LETVGDNFLR HLGIYGYRAG FIRRYVNWQP 200
SPLEHIEMLE QLRVLWYGEK IHVAVAQEVP GTGVDTPEDP STALMKIPGD 250
PGGGDMRDNW RSELYKYKVV KIEPLGVAPT KAKRRVVQRE KRAVGIGALF 300
LGFLGAAGST MGAASMTLTV QARQLLSGIV QQQNNLLRAI EAQQHLLQLT 350
VWGIKQLQAR ILAVERYLKD QQLLGIWGCS GKLICTTAVP WNASWSNKSL 400
EQIWNNMTWM EWDREINNYT SLIHSLIEES QNQQEKNEQE LLELDKWVNR 450
VRQGYSPLSF QTHLPIPRGP DRPEGIEEEG GERDRDRSIR LVIGGDMKDI 500
WRNELFKYKV VRVKPFSVAP TPIARPVIGT GTHREKRAVG LGMLFLGVLS 550
AAGSTMGAAA TALTVQTHSV IKGIVQQQDN LLRAIQAQQE LLRLSVWGIR 600
QLRARLLALE TLIQNQQLLN LWGCKGRLIC YTSVKWNETW RNTTNINQIW 650
GNLTWQEWDQ QIDNVSSTIY EEIQKAQVQQ EQNEKKLLEL DEWASLWNWL 700
DITKWL 706

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1470 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

```
ATGATCGGTG GTGACATGAA AGACATCTGG CGTAACGAAC TGTTCAAATA      50
CAAAGTTGTT CGTGTTAAAC CGTTCTCTGT TGCTCCGACC CCGATCGCTC     100
GTCCGGTTAT CGGTACTGGC ACCCACCGTG AAAAACGTGC TGTAGGTCTG     150
GGTATGCTGT TCCTGGGCGT TCTGTCTGCA GCAGGTTCCA CTATGGGTGC     200
TGCAGCTACC GCTCTGACCG TACAGACCCA CTCTGTTATC AAAGGTATCG     250
TACAGCAGCA GGACAACCTG CTGCGTGCAA TCCAGGCACA GCAGGAACTG     300
CTGCGTCTGT CTGTATGGGG TATCCGTCAG CTGCGTGCTC GTCTGCTGGC     350
ACTGGAAACC CTGATCCAGA ACCAGCAGCT GCTGAACCTG TGGGGCTGCA     400
AAGGTCGTCT GATCTGCTAC ACCTCCGTTA AATGGAACGA AACCTGGCGT     450
AACACCACCA ACATCAACCA GATCTGGGGT AACCTGACCT GGCAGGAATG     500
GGACCAGCAG ATCGACAACG TTTCTTCCAC CATCTACGAA GAAATCCAGA     550
AAGCTCAGGT TCAGCAGGAA CAGAACGAAA AAAAACTGCT GGAACTGGAC     600
GAATGGGCTT CTCTGTGGAA CTGGCTGGAC ATCACCAAAT GGCTGCGTAA     650
CATCCGTCAG GGCTACCAGC CGCTGTCCCT GCAGATCCCG ACCCGTCAGC     700
AGTCTGAAGC TGAAACTCCG GGTCGTACCG GTGAAGGTCC GGGTGGTGGT     750
GACATGCGTG ACAACTGGCG TTCTGAACTG TACAAATACA AAGTTGTTAA     800
AATCGAACCG CTGGGTGTTG CTCCGACTAA AGCTAAACGT CGTGTTGTTC     850
AGCGTGAAAA ACGCGCCGTT GGTATCGGTG CACTGTTCCT GGGTTTCCTG     900
GGTGCTGCTG GTTCTACCAT GGGTGCTGCT TCTATGACCC TGACTGTTCA     950
GGCCCGTCAG CTTCTGTCTG GTATCGTTCA GCAGCAGAAC AATCTGCTGC    1000
GTGCTATCGA AGCTCAGCAG CATCTGCTGC AACTGACCGT TTGGGGTATC    1050
AAACAGCTTC AGGCTCGTAT CCTGGCTGTT GAACGTTACC TGAAAGACCA    1100
GCAGCTGCTG GGTATCTGGG GTTGCTCTGG TAAACTGATC TGCACTACTG    1150
CTGTTCCGTG GAACGCTTCT TGGTCTAACA AATCTCTGGA ACAGATCTGG    1200
AACAACATGA CTTGGATGGA ATGGGACCGT GAAATCAACA ACTACACAAG    1250
CTTGATCCAC TCTCTGATCG AAGAAAGCCA GAACCAGCAG GAAAAAAACG    1300
AACAGGAACT TCTAGAACTG GACAAATGGG TTAACCGTGT TCGTCAGGGT    1350
TACTCTCCGC TGTCTTTCCA GACCCATCTG CCGATCCCGC GTGGTCCGGA    1400
CCGTCCGGAA GGTATCGAAG AAGAAGGCGG CGAACGTGAC CGTGACCGTT    1450
CCATTCGTCT GGTATAATAG                                     1470
```

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 488 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```
MIGGDMKDIW RNELFKYKVV RVKPFSVAPT PIARPVIGTG THREKRAVGL      50
GMLFLGVLSA AGSTMGAAAT ALTVQTHSVI KGIVQQQDNL LRAIQAQQEL     100
LRLSVWGIRQ LRARLLALET LIQNQQLLNL WGCKGRLICY TSVKWNETWR     150
NTTNINQIWG NLTWQEWDQQ IDNVSSTIYE EIQKAQVQQE QNEKKLLELD     200
EWASLWNWLD ITKWLRNIRQ GYQPLSLQIP TRQQSEAETP GRTGEGPGGG     250
DMRDNWRSEL YKYKVVKIEP LGVAPTKAKR RVVQREKRAV GIGALFLGFL     300
GAAGSTMGAA SMTLTVQARQ LLSGIVQQQN NLLRAIEAQQ HLLQLTVWGI     350
```

KQLQARILAV ERYLKDQQLL GIWGCSGKLI CTTAVPWNAS WSNKSLEQIW 400
NNMTWMEWDR EINNYTSLIH SLIEESQNQQ EKNEQELLEL DKWVNRVRQG 450
YSPLSFQTHL PIPRGPDRPE GIEEEGGERD RDRSIRLV 488

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1584 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

ATGAGTTTTG TGGTCATTAT TCCCGCGCGC TACGCGTCGA CGCGTCTGCC 50
CGGTAAACCA TTGGTTGATA TTAACGGCAA ACCCATGATT GTTCATGTTC 100
TTGAACGCGC GCGTGAATCA GGTGCCGAGC GCATCATCGT GGCAACCGAT 150
CATGAGGATG TTGCCCGCGC CGTTGAAGCC GCTGGCGGTG AAGTATGTAT 200
GACGCGCGCC GATCATCAGT CAGGAACAGA ACGTCTGGCG GAAGTTGTCG 250
AAAAATGCGC ATTCAGCGAC GACACGGTGA TCGTTAATGT GCAGGGTGAT 300
GAACCGATGA TCCCTGCGAC AATCATTCGT CAGGTTGCTG ATAACCTCGC 350
TCAGCGTCAG GTGGGTATGA CGACTCTGGC GGTGCCAATC CACAATGCGG 400
AAGAAGCGTT TAACCCGAAT GCGGTGAAAG TGGTTCTCGA CGCTGAAGGG 450
TATGCACTGT ACTTCTCTCG CGCCACCATT CCTTGGGATC GTGATCGTTT 500
TGCAGAAGGC CTTGAAACCG TTGGCGATAA CTTCCTGCGT CATCTTGGTA 550
TTTATGGCTA CCGTGCAGGC TTTATCCGTC GTTACGTCAA CTGGCAGCCA 600
AGTCCGTTAG AACACATCGA AATGTTAGAG CAGCTTCGTG TTCTGTGGTA 650
CGGCGAAAAA ATCCATGTTG CTGTTGCTCA GGAAGTTCCT GGCACAGGTG 700
TGGATACCCC TGAAGATCTC GACCCGTCGA CGAATTCTAT CGGTGGTGAC 750
ATGAAAGACA TCTGGCGTAA CGAACTGTTC AAATACAAAG TTGTTCGTGT 800
TAAACCGTTC TCTGTTGCTC CGACCCCGAT CGCTCGTCCG GTTATCGGTA 850
CTGGCACCCA CCGTGAAAAA CGTGCTGTAG GTCTGGGTAT GCTGTTCCTG 900
GGCGTTCTGT CTGCAGCAGG TTCCACTATG GGTGCTGCAG CTACCGCTCT 950
GACCGTACAG ACCCACTCTG TTATCAAAGG TATCGTACAG CAGCAGGACA 1000
ACCTGCTGCG TGCAATCCAG GCACAGCAGG AACTGCTGCG TCTGTCTGTA 1050
TGGGGTATCC GTCAGCTGCG TGCTCGTCTG CTGGCACTGG AAACCCTGAT 1100
CCAGAACCAG CAGCTGCTGA ACCTGTGGGG CTGCAAAGGT CGTCTGATCT 1150
GCTACACCTC CGTTAAATGG AACGAAACCT GGCGTAACAC CACCAACATC 1200
AACCAGATCT GGGGTAACCT GACCTGGCAG GAATGGGACC AGCAGATCGA 1250
CAACGTTTCT TCCACCATCT ACGAAGAAAT CCAGAAAGCT CAGGTTCAGC 1300
AGGAACAGAA CGAAAAAAAA CTGCTGGAAC TGGACGAATG GGCTTCTCTG 1350
TGGAACTGGC TGGACATCAC CAAATGGCTG CGTAACATCC GTCAGGGCTA 1400
CCAGCCGCTG TCCCTGCAGA TCCCGACCCG TCAGCAGTCT GAAGCTGAAA 1450
CTCCGGGTCG TACCGGTGAA GGTGGCGGTT CTCGCCTGCT GGCTCTGGAA 1500
ACTCTGATTC AGAACCAGCA ACTGCTTAAC CTGTGGGGTT GCAAGGGCCG 1550
CCTGATTTGC TACACTTCTG TAAAATGGTA ATAG 1584

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 526 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

MSFVVIIPAR YASTRLPGKP LVDINGKPMI VHVLERARES GAERIIVATD 50

HEDVARAVEA AGGEVCMTRA DHQSGTERLA EVVEKCAFSD DTVIVNVQGD 100
EPMIPATIIR QVADNLAQRQ VGMTTLAVPI HNAEEAFNPN AVKVVLDAEG 150
YALYFSRATI PWDRDRFAEG LETVGDNFLR HLGIYGYRAG FIRRYVNWQP 200
SPLEHIEMLE QLRVLWYGEK IHVAVAQEVP GTGVDTPEDL DPSTNSIGGD 250
MKDIWRNELF KYKVVRVKPF SVAPTPIARP VIGTGTHREK RAVGLGMLFL 300
GVLSAAGSTM GAAATALTVQ THSVIKGIVQ QQDNLLRAIQ AQQELLRLSV 350
WGIRQLRARL LALETLIQNQ QLLNLWGCKG RLICYTSVKW NETWRNTTNI 400
NQIWGNLTWQ EWDQQIDNVS STIYEEIQKA QVQQEQNEKK LLELDEWASL 450
WNWLDITKWL RNIRQGYQPL SLQIPTRQQS EAETPGRTGE GGGSRLLALE 500
TLIQNQQLLN LWGCKGRLIC YTSVKW 526

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GACCGTCCGG AAGGTATCGA AGAAGAAGGC GGCGAACGTG ACCGTGACCG TTCCATTCGT 60

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATGGAACGGT CACGGTCACG TTCGCCGCCT TCTTCTTCGA TACCTTCCGG ACG 53

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

ATCTCTGGAA CAGATCTGGA 20

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

AGTACTGAAG CAGATTCCAC 20

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CCGTCGTTAC GTCAACTGG 19

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CGCCGTTGGT ATCGGTGC 18

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: XXX base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TACCAGACAG AAGCTGACG 19

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CTTCGATCAG AGAGTGGATC 20

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GACGATCTGC GTTCTCTGTG 20

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1800 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

ATGAGTTTTG TGGTCATTAT TCCCGCGCGC TACGCGTCGA CGCGTCTGCC 50
CGGTAAACCA TTGGTTGATA TTAACGGCAA ACCCATGATT GTTCATGTTC 100
TTGAACGCGC GCGTGAATCA GGTGCCGAGC GCATCATCGT GGCAACCGAT 150
CATGAGGATG TTGCCCGCGC CGTTGAAGCC GCTGGCGGTG AAGTATGTAT 200
GACGCGCGCC GATCATCAGT CAGGAACAGA ACGTCTGGCG GAAGTTGTCG 250
AAAAATGCGC ATTCAGCGAC GACACGGTGA TCGTTAATGT GCAGGGTGAT 300
GAACCGATGA TCCCTGCGAC AATCATTCGT CAGGTTGCTG ATAACCTCGC 350
TCAGCGTCAG GTGGGTATGG CGACTCTGGC GGTGCCAATC CACAATGCGG 400
AAGAAGCGTT TAACCCGAAT GCGGTGAAAG TGGTTCTCGA CGCTGAAGGG 450
TATGCACTGT ACTTCTCTCG CGCCACCATT CCTTGGGATC GTGATCGTTT 500
TGCAGAAGGC CTTGAAACCG TTGGCGATAA CTTCCTGCGT CATCTTGGTA 550
TTTATGGCTA CCGTGCAGGC TTTATCCGTC GTTACGTCAA CTGGCAGCCA 600
AGTCCGTTAG AACACATCGA AATGTTAGAG CAGCTTCGTG TTCTGTGGTA 650
CGGCGAAAAA ATCCATGTTG CTGTTGCTCA GGAAGTTCCT GGCACAGGTG 700
TGGATACCCC TGAAGATCCG TCGACAGCCC TTATGAAGAT CCCCGGCGAC 750
CCGGGTGGTG GTGACATGCG TGACAACTGG CGTTCTGAAC TGTACAAATA 800
CAAAGTTGTT AAAATCGAAC CGCTGGGTGT TGCTCCGACT AAAGCTAAAC 850
GTCGTGTTGT TCAGCGTGAA AAACGCGCCG TTGGTATCGG TGCACTGTTC 900
CTGGGTTTCC TGGGTGCTGC TGGTTCTACC ATGGGTGCTG CTTCTATGAC 950
CCTGACTGTT CAGGCCCGTC AGCTTCTGTC TGGTATCGTT CAGCAGCAGA 1000
ACAATCTGCT GCGTGCTATC GAAGCTCAGC AGCATCTGCT GCAACTGACC 1050
GTTTGGGGTA TCAAACAGCT TCAGGCTCGT ATCCTGGCTG TTGAACGTTA 1100
CCTGAAAGAC CAGCAGCTGC TGGGTATCTG GGGTTGCTCT GGTAAACTGA 1150
TCTGCACTAC TGCTGTTCCG TGGAACGCTT CTTGGTCTAA CAAATCTCTG 1200
GAACAGATCT GGAACAACAT GACTTGGATG GAATGGGACC GTGAAATCAA 1250
CAACTACACA AGCTTGATCC ACTCTCTGAT CGAAGAAAGC CAGAACCAGC 1300
AGGAAAAAAA CGAACAGGAA CTTCTAGAAC TGGACAAATG GGTTAACCGT 1350
GTTCGTCAGG GTTACTCTCC GCTGTCTTTC CAGACCCATC TGCCGATCCC 1400
GCGTGGTCCG GACCGTCCGG AAGGTATCGA AGAAGAAGGC GGCGAACGTG 1450
ACCGTGACCG TTCCATTCGT CTGGTAAACG GTTCTCTGGC TCTGATCTGG 1500
GACGATCTGC GTTCTCTGTG CCTGTTCTCT TACCACCGTC TGCGTGATCT 1550
GCTGCTGATC GTGACTCGTA TCGTTGAACT GCTCGGCCGT CGTGGTTGGG 1600
AAGCTCTGAA ATACTGGTGG AATCTGCTTC AGTACTGGTC CCAGGAACTG 1650
AAAAACTCTG CTGTTTCTCT GCTGAACGCT ACTGCTATCG CTGTTGCTGA 1700
AGGCACCGAT CGTGTTATCG AAGTAGTTCA GGGTGCTTAC CGTGCTATCC 1750
GTCACATTCC GCGTCGTATC CGTCAGGGTC TGGAACGTAT CCTGCTGTAA 1800

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 599 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```
MSFVVIIPAR YASTRLPGKP LVDINGKPMI VHVLERARES GAERIIVATD      50
HEDVARAVEA AGGEVCMTRA DHQSGTERLA EVVEKCAFSD DTVIVNVQGD     100
EPMIPATIIR QVADNLAQRQ VGMATLAVPI HNAEEAFNPN AVKVVLDAEG     150
YALYFSRATI PWDRDRFAEG LETVGDNFLR HLGIYGYRAG FIRRYVNWQP     200
SPLEHIEMLE QLRVLWYGEK IHVAVAQEVP GTGVDTPEDP STALMKIPGD     250
PGGGDMRDNW RSELYKYKVV KIEPLGVAPT KAKRRVVQRE KRAVGIGALF     300
LGFLGAAGST MGAASMTLTV QARQLLSGIV QQQNNLLRAI EAQQHLLQLT     350
VWGIKQLQAR ILAVERYLKD QQLLGIWGCS GKLICTTAVP WNASWSNKSL     400
EQIWNNMTWM EWDREINNYT SLIHSLIEES QNQQEKNEQE LLELDKWVNR     450
VRQGYSPLSF QTHLPIPRGP DRPEGIEEEG GERDRDRSIR LVNGSLALIW     500
DDLRSLCLFS YHRLRDLLLI VTRIVELLGR RGWEALKYWW NLLQYWSQEL     550
KNSAVSLLNA TAIAVAEGTD RVIEVVQGAY RAIRHIPRRI RQGLERILL      599
```

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GACTACTTGT AGCCATTCGT CTGGTAATCG GTGGTGACAT GAAAGAC 47

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

ACAATGATGG TACCTATTAT TCACCGGTAC GAC 33

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

ATTGGTTGAT ATTAACGG 18

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

TCGGTGGTGA CATGAAAGAC 20

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

AAAATAGGCG TATCACGAGG 20

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

ACAATGATGG TACCTATTAC AGCCATTTGG TGATGTCCAG 40

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

TAACGATCAG CTACCGGTGA AGGTCCGGGT GGTGGTGACA TGCGTG 46

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CAAGATGGAT CCTATTATAC CAGACGAATG GAACGGTC 39

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CCGGTGAAGG TGGCGGTTCT CGCCTGCTGG CTCTGGAAAC TCTGATTCAG AACCAGCAAC 60
TGCTTAACCT GTGGGGTTGC AAGGGCCGCC TGATTTGCTA CACTTCTGTA AAATGGTAAT 120
AG 122

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GATCCTATTA CCATTTTACA GAAGTGTAGC AAATCAGGCG GCCCTTGCAA CCCCACAGGT 60
TAAGCAGTTG CTGGTTCTGA ATCAGAGTTT CCAGAGCCAG CAGGCGAGAA CCGCCACCTT 120
CA 122

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 849 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ATGATCGGTG GTGACATGAA AGACATCTGG CGTAACGAAC TGTTCAAATA 50
CAAAGTTGTT CGTGTTAAAC CGTTCTCTGT TGCTCCGACC CCGATCGCTC 100
GTCCGGTTAT CGGTACTGGC ACCCACCGTG AAAAACGTGC TGTAGGTCTG 150
GGTATGCTGT TCCTGGGCGT TCTGTCTGCA GCAGGTTCCA CTATGGGTGC 200
TGCAGCTACC GCTCTGACCG TACAGACCCA CTCTGTTATC AAAGGTATCG 250
TACAGCAGCA GGACAACCTG CTGCGTGCAA TCCAGGCACA GCAGGAACTG 300
CTGCGTCTGT CTGTATGGGG TATCCGTCAG CTGCGTGCTC GTCTGCTGGC 350
ACTGGAAACC CTGATCCAGA ACCAGCAGCT GCTGAACCTG TGGGGCTGCA 400
AAGGTCGTCT GATCTGCTAC ACCTCCGTTA AATGGAACGA AACCTGGCGT 450
AACACCACCA ACATCAACCA GATCTGGGGT AACCTGACCT GGCAGGAATG 500
GGACCAGCAG ATCGACAACG TTTCTTCCAC CATCTACGAA GAAATCCAGA 550
AAGCTCAGGT TCAGCAGGAA CAGAACGAAA AAAAACTGCT GGAACTGGAC 600
GAATGGGCTT CTCTGTGGAA CTGGCTGGAC ATCACCAAAT GGCTGCGTAA 650
CATCCGTCAG GGCTACCAGC CGCTGTCCCT GCAGATCCCG ACCCGTCAGC 700
AGTCTGAAGC TGAAACTCCG GGTCGTACCG GTGAAGGTGG CGGTTCTCGC 750
CTGCTGGCTC TGGAAACTCT GATTCAGAAC CAGCAACTGC TTAACCTGTG 800
GGGTTGCAAG GGCCGCCTGA TTTGCTACAC TTCTGTAAAA TGGTAATAG 849

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 281 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

```
MIGGDMKDIW RNELFKYKVV RVKPFSVAPT PIARPVIGTG THREKRAVGL   50
GMLFLGVLSA AGSTMGAAAT ALTVQTHSVI KGIVQQQDNL LRAIQAQQEL  100
LRLSVWGIRQ LRARLLALET LIQNQQLLNL WGCKGRLICY TSVKWNETWR  150
NTTNINQIWG NLTWQEWDQQ IDNVSSTIYE EIQKAQVQQE QNEKKLLELD  200
EWASLWNWLD ITKWLRNIRQ GYQPLSLQIP TRQQSEAETP GRTGEGGGSR  250
LLALETLIQN QQLLNLWGCK GRLICYTSVK W                      281
```

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

```
ACGTTCGCCG CCTTCTTCTT CG                                 22
```